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=> e bjorck lars/au

E1	446	BJORCK L/AU
E2	7	BJORCK L H/AU

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E3           75 --> BJORCK LARS/AU
E4            4     BJORCK LARS HENRIK/AU
E5            1     BJORCK LENART/AU
E6           15     BJORCK LENNART/AU
E7            9     BJORCK LINNE A/AU
E8            2     BJORCK LINNE A K/AU
E9            4     BJORCK LINNE AGNETA/AU
E10          27     BJORCK M/AU
E11           3     BJORCK MARTIN/AU
E12          52     BJORCK P/AU

=> s e1-e4

L1          532 ("BJORCK L"/AU OR "BJORCK L H"/AU OR "BJORCK LARS"/AU
OR "BJORCK
                LARS HENRIK"/AU)

=> e sjobring ulf/au

E1            1     SJOBRING N P/AU
E2          103     SJOBRING U/AU
E3           48 --> SJOBRING ULF/AU
E4            1     SJOBROG S/AU
E5            1     SJOBU L/AU
E6            1     SJOBURG KNUT/AU
E7            2     SJODAHL C/AU
E8            1     SJODAHL C J/AU
E9            1     SJODAHL CATHARINA/AU
E10           4     SJODAHL E/AU
E11           3     SJODAHL E J/AU
E12           1     SJODAHL ERIC/AU

=> s e2-e3

L2          151 ("SJOBRING U"/AU OR "SJOBRING ULF"/AU)

=> s l1-l2

L3          614 (L1 OR L2)

=> s l3 and immunoglobulin?

L4          233 L3 AND IMMUNOGLOBULIN?

=> s l4 and (protein l or light chain or hybrid)

   6 FILES SEARCHED...
L5          102 L4 AND (PROTEIN L OR LIGHT CHAIN OR HYBRID)

=> s l5 and domain?

L6           62 L5 AND DOMAIN?

=> dup rem l6

PROCESSING COMPLETED FOR L6
L7            24 DUP REM L6 (38 DUPLICATES REMOVED)

=> d bib ab 1-24
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L7 ANSWER 1 OF 24 WPIDS COPYRIGHT 2002 DERWENT INFORMATION LTD
DUPLICATE
1
AN 2001-398077 [42] WPIDS
DNC C2001-121057
TI Novel vaccine composition comprising **protein L**, its
analog or fragment, useful for enhancing immune response to an
antigen in
an individual.
DC B04 D16
IN **BJORCK, L**; LEANDERSON, T; WICK, M J
PA (ACTI-N) ACTINOVA LTD
CYC 94
PI WO 2001043769 A2 20010621 (200142)* EN 25p
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU
MC MW MZ
NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ
DE DK DM
DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP
KR KZ LC
LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO
RU SD SE
SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
AU 2001021993 A 20010625 (200162)
ADT WO 2001043769 A2 WO 2000-GB4830 20001215; AU 2001021993 A AU
2001-21993
20001215
FDT AU 2001021993 A Based on WO 200143769
PRAI GB 1999-29937 19991217
AB WO 200143769 A UPAB: 20010726
NOVELTY - A vaccine composition (I) comprising **protein L**
, its analog or fragment, coupled to a heterologous antigen, is
new.
ACTIVITY - Immunosuppressive.
MECHANISM OF ACTION - Vaccine (claimed). Preparations of
Protein L B1-B4, B1-B1 or B1 were incubated with
splenocytes from mice for 24, 48 or 72 hours in the presence or
absence of
10 micro g/ml PMB. The level of surface expression of the
co-stimulatory
molecules B7-1, B7-2 and CD40, as well as MHC-I and MHC-II
expression on B
cells, was analyzed by fluorescence-activated cell sorting
(FACS). The
result showed that **protein L** B1-B4 (5 micro g) as
well as B1-B1 (10 micro g) and B1 (10 micro g) caused up
regulation of
B7-2 expression on gated B220+ cells, with the most dramatic
effect
occurring with B1-B4. B1-B4 also upregulated CD40 and MHC-I
expression,
but had no apparent effect on MHC-II. A slight influence of
B1-B1 and B1
on surface expression of CD40 and MHC-I was detectable.
USE - (I) is useful for enhancing an immune response to an
antigen in

an individual (claimed). **Protein L** is useful for treating autoimmune diseases.
Dwg.0/5

L7 ANSWER 2 OF 24 USPATFULL
AN 2001:82536 USPATFULL
TI Treatment of bacterial infections
IN **Bjorck, Lars**, Lund, Sweden
Sjorbring, Ulf, Lund, Sweden
Nasr, Abdelhakim Ben, Cambridge, United Kingdom
Olsen, Arne, Bjarred, Sweden
Herwald, Heiko, Malmo, Sweden
Muller-Esterl, Werner, Mainz, Germany, Federal Republic of
Mattsson, Eva, Lund, Sweden
PA Actinova Limited, United Kingdom (non-U.S. corporation)
PI US 6242210 B1 20010605
AI US 1999-258688 19990226 (9)
RLI Continuation of Ser. No. US 194098
DT Utility
FS Granted
EXNAM Primary Examiner: Leary, Louise N.
LREP Seed IP Law Group
CLMN Number of Claims: 5
ECL Exemplary Claim: 1
DRWN 40 Drawing Figure(s); 18 Drawing Page(s)
LN.CNT 2437
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB An assay for compounds useful in the treatment of a bacterial induced
coagulation disorder has the following steps:

a) incubating a plasma sample with a strain of bacteria;

b) adding a compound to be assayed to the plasma sample before, during
or after step (a);

c) conducting an activated partial thromboplastin time test;

d) determining the clotting time.

L7 ANSWER 3 OF 24 USPATFULL
AN 2001:59866 USPATFULL
TI Use of kinin antagonists for preparing a pharmaceutical composition for
treating bacterial infections
IN **Bjorck, Lars**, Lund, Sweden
Sjobring, Ulf, Lund, Sweden
Nasr, Abdelhakim Ben, Cambridge, United Kingdom
Olsen, Arne, Lund, Sweden
Herwald, Heiko, Lund, Sweden
Muller-Esterl, Werner, Mainz, Germany, Federal Republic of
PA Actinova Limited, Cambridge, United Kingdom (non-U.S. corporation)
PI US 6221845 B1 20010424
WO 9744353 19971127
AI US 1999-194098 19990625 (9)
WO 1997-SE825 19970520
19990625 PCT 371 date

19990625 PCT 102(e) date
PRAI SE 1996-1901 19960520
DT Utility
FS Granted
EXNAM Primary Examiner: Weddington, Kevin E.
LREP Seed IP Law Group PLLC
CLMN Number of Claims: 4
ECL Exemplary Claim: 1
DRWN 27 Drawing Figure(s); 13 Drawing Page(s)
LN.CNT 1607
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Kinin antagonists, especially bradykinin antagonists, can be used for
treating bacterial infections, in particular infections caused by
bacteria belonging to the genera Streptococcus, Escherichia, Salmonella,
Staphylococcus, Klebsiella, Moracella, Haemophilus and Yersinia.

L7 ANSWER 4 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 2
AN 2001220077 EMBASE
TI **Immunoglobulin**-binding **domains** of peptostreptococcal **protein L** enhance vaginal colonization of mice by Streptococcus gordonii.
AU Ricci S.; Medaglini D.; Marcotte H.; Olsen A.; Pozzi G.; **Bjorck L.**
CS S. Ricci, Department of Molecular Biology, Section for Microbiology,
University of Siena, 53100 Siena, Italy. riccisus@unisi.it
SO Microbial Pathogenesis, (2001) 30/4 (229-235).
Refs: 41
ISSN: 0882-4010 CODEN: MIPAEV
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
005 General Pathology and Pathological Anatomy
LA English
SL English
AB **Protein L**, an **immunoglobulin**-binding protein of some strains of the anaerobic bacterium Peptostreptococcus magnus, has been hypothesized to be a virulence determinant in bacterial vaginosis. In order to investigate the role of **protein L** in peptostreptococcal virulence, the Ig-binding **domains** of **protein L** were expressed at the surface of the human oral commensal Streptococcus gordonii. Recombinant streptococci were used in vaginal colonization experiments, and **protein L** -expressing S. gordonii demonstrated enhanced ability to colonize the vaginal mucosa. Compared to the control strain, they also persisted for a longer period in the murine vagina. .COPYRGT. 2001 Academic Press.

L7 ANSWER 5 OF 24 USPATFULL

AN 1999:124726 USPATFULL
TI **Protein L** and **hybrid** proteins thereof
IN **Bjorck, Lars**, Sodra Sandby, Sweden
Sjobring, Ulf, Lund, Sweden
PA Actinova Ltd., Lund, Sweden (non-U.S. corporation)
PI US 5965390 19991012
AI US 1997-795475 19970211 (8)
RLI Division of Ser. No. US 1994-325278, filed on 26 Oct 1994
PRAI SE 1992-1331 19920428
DT Utility
FS Granted
EXNAM Primary Examiner: Degen, Nancy
LREP Seed and Berry LLP
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN 17 Drawing Figure(s); 17 Drawing Page(s)
LN.CNT 1305
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to sequences of **protein L** which bind to light chains of **immunoglobulins**. The invention also relates to **hybrid** proteins thereof which are able to bind to both light and heavy chains of **immunoglobulin** G, in particular protein LG. The invention also relates to DNA-sequences which code for the proteins, vectors which include such DNA-sequences, host cells which have been transformed with the vectors, methods for producing the proteins, reagent appliances for separation and identification of **immunoglobulins**, compositions and pharmaceutical compositions and pharmaceutical compositions which contain the proteins.

L7 ANSWER 6 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 3
AN 1998416862 EMBASE
TI Protein LA, a novel **hybrid** protein with unique single-chain Fv antibody- and Fab-binding properties.
AU Svensson H.G.; Hoogenboom H.R.; **Sjobring U.**
CS U. Sjobring, Department of Medical Microbiology, Solvegatan 23, S-22362 Lund, Sweden. ulf.sjobring@mmb.lu.se
SO European Journal of Biochemistry, (1 Dec 1998) 258/2 (890-896). Refs: 44
ISSN: 0014-2956 CODEN: EJBCAI
CY United Kingdom
DT Journal; Article
FS 026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LA English
SL English
AB Existing Ig-binding proteins all suffer from limitations in their binding spectrum. In the pursuit of the ultimate, non-restricted, Ig-binding protein, we have constructed the **hybrid** protein LA, by fusing four of the Ig.kappa. **light-chain**-binding **domains** of peptostreptococcal **protein L** with four of the IgGFc- and Fab-binding regions of staphylococcal protein A.

Ligand-blot experiments demonstrated that the L and the A components were both functional in the **hybrid**, as the protein was shown to bind purified x light chains and IgGFc. Protein LA bound human Ig of different classes and IgG from a wide range of mammalian species. IgG, IgM and IgA were purified from human serum and saliva by affinity chromatography on protein LA agarose. Similarly, single-chain Fv (scFv) antibodies carrying the .kappa. **light-chain** variable **domain** or expressing the V(H)III (variable **domain** of the heavy chain of Ig) determinant, were efficiently purified on immobilized protein LA. As judged by surface plasmon resonance (SPR), protein LA showed enhanced affinity for all tested ligands, including several scFv antibodies, compared with proteins L and A alone. SPR analysis also demonstrated that binding of a ligand to one of the components in protein LA did not affect the ability of the **hybrid** protein to interact simultaneously with a ligand for the other component. The antigen-binding capacity of a .kappa.-expressing scFv antibody was unaffected by the interaction with protein LA, whereas the binding of a V(H)III-expressing scFv antibody to its antigen was, unexpectedly, blocked by protein A and protein LA. Together, these data demonstrate that protein LA represents a highly versatile Ig-binding molecule.

L7 ANSWER 7 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 4
AN 97086135 EMBASE
DN 1997086135
TI Solution structure of the albumin-binding GA module: A versatile bacterial protein **domain**.
AU Johansson M.U.; De Chateau M.; Wikstrom M.; Forsen S.; Drakenberg T.; **Bjorck L.**
CS M.U. Johansson, Department of Physical Chemistry 2, Chemical Center Lund University, POB 124, S-221 00 Lund, Sweden
SO Journal of Molecular Biology, (1997) 266/5 (859-865).
Refs: 40
ISSN: 0022-2836 CODEN: JMOBAK
CY United Kingdom
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English
AB The albumin-binding GA module is found in a family of surface proteins of

different bacterial species. It comprises 45 amino acid residues and represents the first known example of contemporary module shuffling. Using 1H NMR spectroscopy we have determined the solution structure of the GA module from protein PAB, a protein of the anaerobic human commensal and pathogen Peptostreptococcus magnus. This structure, the first three-dimensional structure of an albumin-binding protein **domain** described, was shown to be composed of a left-handed three-helix-bundle. Sequence differences between GA modules with different affinities for albumin indicated that a conserved region in the C-terminal part of the second helix and the flexible sequence between helices 2 and 3 could contribute to the albumin-binding activity. The effect on backbone amide proton exchange rates upon binding to albumin support this assumption. The GA module has a fold that is strikingly similar to the **immunoglobulin**-binding **domains** of staphylococcal protein A but it shows no resemblance to the fold shared by the **immunoglobulin**-binding **domains** of streptococcal protein G and peptostreptococcal **protein L**. When the gene sequences, binding properties and thermal stability of these four **domains** are analysed in relation to their global folds an evolutionary pattern emerges. Thus, in the evolution of novel binding properties mutations are allowed only as long as the energetically favourable global fold is maintained.

L7 ANSWER 8 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 5
AN 97208477 EMBASE
DN 1997208477
TI NMR analysis of the interaction between **protein L** and Ig light chains.
AU Enokizono J.; Wikstrom W.; **Sjobring U.**; **Bjorck L.**; Forsen S.; Arata Y.; Kato K.; Shimada I.
CS W. Wikstrom, Department of Physical Chemistry 2, Lund University, Lund, Sweden
SO Journal of Molecular Biology, (1997) 270/1 (8-13).
Refs: 39
ISSN: 0022-2836 CODEN: JMOBAK
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LA English
SL English
AB **Protein L** is a cell wall protein expressed by some strains of the anaerobic bacterial species Peptostreptococcus magnus. It

binds to **immunoglobulin** (Ig) light chains predominantly of the .kappa. subtype from a wide range of animal species. This binding is mediated by five highly homologous repeats designated as B1-B5, each of which comprises 72 to 76 amino acid residues. The fold of the Ig **light chain**-binding B1 **domain** of **protein L** has previously been shown to comprise an .alpha.-helix packed against a four-stranded .beta.-sheet. The Ig-binding region of the **protein L domain** involves most of the residues in the second .beta.-strand, the C-terminal residues of the .alpha.-helix, and residues in the loop connecting the .alpha.-helix with the third .beta.-strand. In the present study, we have identified the **protein L**-binding site of an Ig **light chain** by use of stable isotope-assisted NMR spectroscopy. The **light chain** of a murine monoclonal anti-17.alpha.-hydroxyprogesterone Fab fragment (IgG2b, .kappa.) was selectively labeled with 13C at carbonyl groups of Ala, Arg, Cys, Ile, Lys, Met, Phe, Trp, or Tyr. The residues in which the carbonyl 13C chemical shift was significantly perturbed upon binding of the **protein L** B1 **domain** were preferentially found in the second .beta.-strand of the variable .kappa. **domain** and parts of its flanking .beta.-strands. None of these residues were affected by the addition of the antigen against which the monoclonal Fab fragment is directed. Therefore, we conclude that **protein L** binds to the outer surface of the framework region of the V(L) **domain**, primarily involving the V(L) second strand, and that this binding is independent of antigen-binding. The present NMR data, in combination with sequence comparisons between .kappa. light chains with and without **protein L** affinity, suggest that the amino acid substitutions at positions 9, 20, and/or 74 of the .kappa. light chains could crucially affect the interaction between **protein L** and the V(L) **domain**.

L7 ANSWER 9 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 6
AN 96327955 EMBASE
DN 1996327955
TI Protein PAB, an albumin-binding bacterial surface protein promoting growth and virulence.
AU De Chateau M.; Holst E.; **Bjorck L.**
CS Department of Cell/Molecular Biology, Lund University, P.O. Box 94,S-221 00 Lund, Sweden
SO Journal of Biological Chemistry, (1996) 271/43 (26609-26615). ISSN: 0021-9258 CODEN: JBCHA3

CY United States
DT Journal; Article
FS 004 Microbiology
010 Obstetrics and Gynecology
026 Immunology, Serology and Transplantation
LA English
SL English
AB The anaerobic bacterium Peptostreptococcus magnus is a human commensal and pathogen. Previous work has shown that strains of P. magnus isolated from patients with gynecological disease (vaginosis) frequently express an **immunoglobulin** (Ig) **light chain**-binding protein called **protein L**. Here we report that strains isolated from localized suppurative infections bind human serum albumin (HSA), whereas commensal isolates bind neither Ig nor HSA. The HSA-binding protein PAB was extracted from the bacterial surface or isolated from the culture supernatant of the P. magnus strain ALBS. Protein PAB was shown to have two homologous HSA-binding **domains**, GA and uGA. GA is absent in the sequence of a related protein from another P. magnus strain and shows a high degree of homology to the HSA-binding **domains** of streptococcal protein G. Therefore GA is believed to have recently been shuffled as a module from genes of other bacterial species into the protein PAB gene. This GA module was shown to exhibit a much higher affinity for HSA than uGA and was also found to be present in all of the isolates tested from localized suppurative infections, indicating a role in virulence. Moreover, when peptostreptococci or streptococci expressing the GA module were grown in the presence of HSA, the growth rate was substantially increased. Thus, the HSA binding activity of the GA module adds selective advantages to the bacteria, which increases their virulence in the case of P. magnus strains.

L7 ANSWER 10 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 7
AN 96248384 EMBASE
DN 1996248384
TI Identification of interdomain sequences promoting the intronless evolution of a bacterial protein family.
AU De Chateau M.; **Bjorck L.**
CS Section for Molecular Pathogenesis, Department of Cell/Molecular Biology, Lund University, P.O. Box 94,S-221 00 Lund, Sweden
SO Proceedings of the National Academy of Sciences of the United States of

America, (1996) 93/16 (8490-8495).
ISSN: 0027-8424 CODEN: PNASA6
CY United States
DT Journal; Article
FS 004 Microbiology
LA English
SL English
AB In the evolution of eukaryotic genes, introns are believed to have played a major role in increasing the probability of favorable duplication events, chance recombinations, and exon shuffling resulting in functional **hybrid** proteins. As a rule, prokaryotic genes lack introns, and the examples of prokaryotic introns described do not seem to have contributed to gene evolution by exon shuffling. Still, certain protein families in modern bacteria evolve rapidly by recombination of genes, duplication of functional **domains**, and as shown for protein PAB of the anaerobic bacterial species Peptostreptococcus magnus, by the shuffling of an albumin-binding protein module from group C and G streptococci. Characterization of a protein PAB- related gene in a P. magnus strain with less albumin-binding activity revealed that the shuffled module was missing. Based on this fact and observations made when comparing gene sequences of this family of bacterial surface proteins interacting with albumin and/or **immunoglobulin**, a model is presented that can explain how this rapid intronless evolution takes place. A new kind of genetic element is introduced: the recer sequence promoting interdomain, in frame recombination and acting as a structureless flexibility-promoting spacer in the corresponding protein. The data presented also suggest that antibiotics could represent the selective pressure behind the shuffling of protein modules in P. magnus, a member of the indigenous bacterial flora.

L7 ANSWER 11 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 8
AN 96295065 EMBASE
DN 1996295065
TI Characterization of the binding properties of protein LG, an **immunoglobulin**-binding **hybrid** protein.
AU Kihlberg B.-M.; Sjoholm A.G.; **Bjorck L.**; **Sjobring U.**
CS Department of Medical Microbiology, Lund University,S-223 62 Lund, Sweden
SO European Journal of Biochemistry, (1996) 240/3 (556-563).
ISSN: 0014-2956 CODEN: EJBCAI
CY Germany
DT Journal; Article
FS 026 Immunology, Serology and Transplantation

029 Clinical Biochemistry
LA English
SL English
AB Protein LG is a 50-kDa **hybrid** molecule containing four Ig-**light-chain**-binding **domains** from **protein L** of Peptostreptococcus magnus and two IgG-Fc binding repeats from streptococcal protein G. Here we analyse the binding of protein LG to Ig from several mammalian species. Protein LG was shown to bind human IgG of all subclasses and other Ig classes that carry K chains. The binding to human IgG was only marginally influenced by changes in temperature (4-37.degree.C) or salt concentration (0-1.6 M), and was stable over a wide pH range (pH 4-10). Protein LG bound to Ig from 11 of 12 mammalian species, including those of rabbit, mouse and rat. The affinity constants obtained for the interactions between protein LG and polyclonal IgG from rabbit (4.0 x 109 M-1), mouse (1.7 x 109 M-1) and rat (1.3 X 109 M-1) were similar to the value previously reported for the interaction between the **hybrid** protein and human polyclonal IgG (5.9 x 109M-1. The interaction between protein LG and a mouse IgG mAb was not infuenced by the presence of the specific protein antigen, nor was the binding of this antibody to its ligand affected by protein LG. Inhibition experiments demonstrated that the Ig-binding site of one of the fusion partners retained its ligand-binding capacity when the other component was occupied. Protein LG selectively absorbed 85-90% of the total Ig present in human and rabbit sera and 75-80% of the Ig in sera from mouse and rat. Human serum depleted of C1q, factor D and properdin and preabsorbed by protein LG could be used as a source for other complement factors. These data demonstrate that protein LG is a very versatile Ig-binding protein.

L7 ANSWER 12 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 95261390 EMBASE
DN 1995261390
TI Multiple ligand interactions for bacterial **immunoglobulin**-binding proteins on human and murine cells of the hematopoetic lineage.
AU Axcrona K.; **Bjorck L.**; Leanderson T.
CS The Immunology Unit, University of Lund, Solvegatan 21,S-223 62 Lund, Sweden
SO Scandinavian Journal of Immunology, (1995) 42/3 (359-367).

ISSN: 0300-9475 CODEN: SJIMAX
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LA English
SL English
AB A group of bacterial Ig-binding surface proteins were studied: protein H and M1 are from Streptococcus pyogenes and interact with IgG, **protein L** is expressed by Peptostreptococcus magnus and shows affinity for Ig light chains, whereas protein LG is a chimeric construction combining the binding properties of **protein L** with the IgG-binding activity of protein G from group C and G streptococci. Proteins L and H coupled to Sepharose were mitogenic for human peripheral blood lymphocytes (PBL) and mouse splenic B cells, but not when added in soluble form. Differentiation to Ig secretion was induced by protein H-Sepharose in mouse splenic B cells but not in human PBLs. In FAGS analysis FITC-labelled protein H stained virtually all CD19+ cells in human peripheral blood as well as a majority of the CD3+ population. **Protein L** bound the majority of the CD19+ population, but also a fraction of the CD19-/CD3 population. Protein M1 was not mitogenic but stained the entire CD19+ population and 70% of the CD3+ population. Identical staining patterns were observed with mouse splenocytes using B220 and T-cell receptor as lineage markers. The chimeric protein LG was a potent mitogen for mouse splenic B cells when added either coupled to Sepharose or in soluble form. In addition, protein LG induced differentiation to Ig secretion of the responding mouse splenic B cells. In FAGS analysis, protein LG stained the entire CD19+ and the majority of the CD19-/CD3 lymphocyte population as well as all B220+ mouse splenocytes and a fraction of the splenic T cells. These data indicate that the bacterial proteins studied interact with surface structures of several leucocyte populations and can hence interfere with the immune system at multiple levels.

L7 ANSWER 13 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 9
AN 95224312 EMBASE
DN 1995224312
TI Mapping of the **immunoglobulin light chain**

-binding site of **protein L**.
AU Wikstrom M.; **Sjobring U.**; Drakenberg T.; Forsen S.; **Bjorck L.**
CS Department of Physical Chemistry 2, Lund University,Lund, Sweden
SO Journal of Molecular Biology, (1995) 250/2 (128-133).
ISSN: 0022-2836 CODEN: JMOBAK
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LA English
SL English
AB **Protein L** is a cell surface protein expressed by some strains of the anaerobic bacterial species Peptostreptococcus magnus. The molecule binds specifically and with high affinity to **immunoglobulins** (Ig) of a wide range of animal species. The Ig-binding activity is mediated through five highly homologous **domains**, each 72 to 76 amino acid residues long, which interact with framework regions in the variable **domain** of Ig light chains. The interaction does not interfere with the antigen binding capacity of the antibody. The fold of the Ig **light chain** -binding **domains** of **Protein L** is comprised of an .alpha.-helix packed against a four stranded .beta.-sheet and is similar to the fold of the IgG heavy chain-binding **domains** of streptococcal protein G, despite the fact that the two proteins show no significant sequence homology. In the present work, heteronuclear NMR spectroscopy has been utilized to define the interaction between the N-terminal Ig-binding **domain** of **Protein L** and the variable **domain** of a human Ig kappa **light chain**. The Ig-binding region of the **Protein L** **domain** involves most of the residues in the second .beta.-strand, the C-terminal residues of the .alpha.-helix and the loop connecting the .alpha.-helix with the third .beta.-strand. The Ig **light chain**-binding surface of **Protein L** thus resembles the surface of Protein G which binds to the C.gamma.1 **domain** of IgG, but is different from the portion of Protein G involved in the contact with the C.gamma.2-C.gamma.3 interface region. The data suggest that the global fold shared by the Ig-binding **domains** of Proteins L and G provide bacteria with a flexible template for the evolution of surface structures capable of interacting with different conserved parts of Ig molecules of the infected host.

L7 ANSWER 14 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 10
AN 95249085 EMBASE
DN 1995249085
TI High level expression of **protein L**, an

immunoglobulin-binding protein, in Escherichia coli.
AU Tocaj A.; **Sjobring U.**; **Bjorck L.**; Holst O.
CS Dept. of Biotechnology, Chemical Center, Lund University, P.O. Box
124,S-221 00 Lund, Sweden
SO Journal of Fermentation and Bioengineering, (1995) 80/1 (1-5).
ISSN: 0922-338X CODEN: JFBIEX
CY Japan
DT Journal; Article
FS 027 Biophysics, Bioengineering and Medical Instrumentation
LA English
SL English
AB A high level expression system for production of an **immunoglobulin**
- binding protein, in Escherichia coli was studied. The protein, called
protein L(I-IV), consists of four **immunoglobulin**
-binding **domains** of the native **protein L**. A
simple fed-batch cultivation strategy was used to investigate the influence of different induction times on cell growth, viability, acetic
acid formation and product formation. Induction allowing product formation
for several hours, i.e., in this case in early exponential phase, was most
favorable in terms of product yields. The highest specific yield obtained
was 150 mg protein per gram cell dry weight (dw), corresponding to 360 mg
per liter broth. The leakage of product into the media was less than 5%.
Induction in early exponential phase lead to the highest amount of acetic
acid, 1.47 g/g dw. Viability decreased significantly after induction.

L7 ANSWER 15 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 11
AN 94380159 EMBASE
DN 1994380159
TI Three-dimensional solution structure of an **immunoglobulin light chain**- binding **domain** of **protein L**. Comparison with the IgG-binding **domains** of protein G.
AU Wikstrom M.; Drakenberg T.; Forsen S.; **Sjobring U.**; **Bjorck L.**
CS Department of Physical Chemistry 2, Lund University,Lund, Sweden
SO Biochemistry, (1994) 33/47 (14011-14017).
ISSN: 0006-2960 CODEN: BICHAW
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English
AB **Protein L** is a multidomain protein expressed at the surface of some strains of the anaerobic bacterial species Peptostreptococcus magnus. It has affinity for **immunoglobulin** (Ig) through interaction with framework structures in the
iable Ig
light chain domain. The Ig-binding activity is

located to five homologous repeats called B1-B5 in the N-terminal part of the protein. We have determined the three-dimensional solution structure of the 76 amino acid residue long B1 **domain** using NMR spectroscopy and distance geometry-restrained simulated annealing. The **domain** is composed of a 15 amino acid residue long disordered N-terminus followed by a folded portion comprising an .alpha.-helix packed against a four-stranded .beta.-sheet. These secondary structural elements are well determined with a backbone atomic root mean square deviation from their mean of 0.54 .ANG.. The B **domains** of **protein L** show very limited sequence homology to the **domains** of streptococcal protein G interacting with the heavy chains of IgG. However, despite this fact, and their different binding properties, the fold of the B1 **domain** was found to be similar to the fold of the IgG-binding protein G **domains** [Wikstrom, M., Sjobring, U., Kastern, W., Bjorck, L., Drakenberg, T., and Forsen, S. (1993) Biochemistry 32, 3381-3386]. In the present study, the solution structure of the B1 **domain** enabled a more detailed comparison which can explain the different Ig-binding specificities of these two bacterial surface proteins. Among the differences observed, the .alpha.-helix orientation is the most striking. Thus, in the B1 **domain** of **protein L** the helix is almost parallel to the .beta.-sheet, whereas in the protein G **domains** the helix runs diagonally across the sheet.

L7 ANSWER 16 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 12
AN 94206234 EMBASE
DN 1994206234
TI Protein PAB, a mosaic albumin-binding bacterial protein representing the first contemporary example of module shuffling.
AU De Chateau M.; **Bjorck L.**
CS Dept. of Medical/Physiological Chem., Lund University, P.O. Box 94,S-221 00 Lund, Sweden
SO Journal of Biological Chemistry, (1994) 269/16 (12147-12151). ISSN: 0021-9258 CODEN: JBCHA3
CY United States
DT Journal; Article
FS 004 Microbiology
LA English
SL English
AB Some strains of the anaerobic human commensal and pathogen Peptostreptococcus magnus bind human serum albumin (HSA), whereas other strains of this species express **protein L**, an **immunoglobulin light chain**- binding surface protein. A novel HSA-binding protein called protein PAB was purified in

one step from the culture supernatant of an HSA-binding strain of P. magnus by affinity chromatography on HSA-Sepharose. The apparent size of the molecule was 47 kDa on SDS-polyacrylamide gel electrophoresis. Amino acid sequence analysis of protein PAB demonstrated that the 4 NH2-terminal residues were identical to the corresponding sequence in **protein L**. In a polymerase chain reaction, oligonucleotides based on extragenic 5'- and 3'- end sequences of the **protein L** gene generated a product of the expected size: 1.3 kilobase pairs. A recombinant protein with retained albumin binding capacity was expressed in Escherichia coli, and the nucleotide sequence of the protein PAB gene was determined. The structural gene is 1161 nucleotides long, corresponding to a preprotein of 387 amino acids and a molecular mass of 43,043 Da. Unlike most other Gram-positive bacterial surface proteins described, protein PAB contains no internal homologies. However, substantial homologies were found to both proteins L and G (the IgG- and HSA-binding surface protein of group C and G streptococci). The derived amino acid sequence of the 135-base pair-long region homologous to protein G corresponds to the HSA-binding **domain** of that protein, and in protein PAB, this region is inserted between sequences showing extensive homology to COOH-terminal regions of peptostreptococcal **protein L**. This mosaic organization of protein PAB demonstrates that the molecule is a product of intergenic interspecies recombination of a functional **domain** into a common framework for peptostreptococcal surface proteins. Such an interspecies exchange of a functional protein module has previously not been described in prokaryotic cells.

L7 ANSWER 17 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 13
AN 95022104 EMBASE
DN 1995022104
TI On the interaction between single chain Fv antibodies and bacterial **immunoglobulin**-binding proteins.
AU Akerstrom B.; Nilson B.H.K.; Hoogenboom H.R.; **Bjorck L.**
CS Dept Medical/Physiological Chemistry, Lund University, P.O. Box 94,S-221 00 Lund, Sweden
SO Journal of Immunological Methods, (1994) 177/1-2 (151-163). ISSN: 0022-1759 CODEN: JIMMBG
CY Netherlands
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
029 Clinical Biochemistry

LA English
SL English
AB Using four bacterial **immunoglobulin**-binding proteins, we have analyzed the binding characteristics of a panel of 34 human single chain Fv antibodies, expressed in E. coli and with known specificity and sequence. Several of the single chain Fv antibodies showed affinity for staphylococcal protein A and peptostreptococcal **protein L**, but not for the streptococcal proteins G or H. The affinity of the binding was higher for **protein L** (4.5 and 1.4 x 109 M-1) than for protein A (7.7 and 6.7 x 108 M-1), using the two single chain Fv antibodies displaying the strongest binding activity to these ligands. The binding was shown to be specific by Western blotting, and the single chain Fv antibodies could be purified from crude bacterial culture media by affinity chromatography on **protein L**- or A-Sepharose. Protein A, which has affinity for the V(H) **domain** of the scFv antibodies, was tested against scFv antibodies containing V(H)1, V(H)3, V(H)4 and V(H)5 **domains**, and its binding was restricted to approximately half of the scFv antibodies with a V(H)3 **domain**. **Protein L**, which has affinity for the V(L) **domain**, was tested against .kappa.1, .kappa.4, .lambda.1, .lambda.2 and .lambda.3 **domains**, and it bound all .kappa.1 **domains**, one .lambda.2 and one .lambda.3 **domain**. Comparison of the amino acid sequences of binding and non-binding V(L) **domains** demonstrated that amino acid residues crucial to the binding of **protein L** were distributed over a large area outside the hypervariable antigen-binding regions.

L7 ANSWER 18 OF 24 MEDLINE
AN 95254583 MEDLINE
DN 95254583 PubMed ID: 7736533
TI Recombinant proteins L and LG. Two new tools for purification of murine antibody fragments.
AU Vola R; Lombardi A; Tarditi L; Zaccolo M; Neri D; **Bjorck L**; Mariani M
CS Biochemical Oncology Labs., SORIN Biomedica, Saluggia VC, Italy.
SO CELL BIOPHYSICS, (1994) 24-25 27-36.
Journal code: CQC; 8002185. ISSN: 0163-4992.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199506
ED Entered STN: 19950615
Last Updated on STN: 19950615
Entered Medline: 19950602
AB Several bacterial cell wall proteins, like proteins A and G, with valuable affinity for **immunoglobulins** have been discovered and are

currently employed in immunological techniques. In 1988, **protein L**, a bacterial cell wall protein with Ig-binding capacity, was isolated from the anaerobic bacterial species Peptostreptococcus magnus.

Binding data with **immunoglobulin** fragments suggested that **protein L** could selectively bind the variable region of human kappa light chains. More recently a recombinant LG fusion protein was expressed in E. coli containing four repeated Ig-binding **domains** of **protein L** (fragment B1-4) and two IgG Fc-binding protein G **domains** (fragment CDC). Recombinant L and LG proteins were tested in the purification of murine monoclonal IgG and their fragments. After affinity-constant evaluation in different buffer systems, high-pressure affinity-chromatography columns were prepared by coupling the proteins to Affi-prep 10 resin and tested with eight different murine monoclonal antibodies and their fragments of various isotypes. Affinity-chromatography experiments confirming radioimmunoassay results showed 75% fragment-binding capacity of **protein L** and 100% of protein LG. These results evidenced protein LG as the most powerful Ig-binding tool so far described. Therefore, application of these proteins may be suggested in the purification of murine **immunoglobulins** and their fragments, including the engineered ones.

L7 ANSWER 19 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 14
AN 93126906 EMBASE
DN 1993126906
TI Proton nuclear magnetic resonance sequential assignments and secondary structure of an **immunoglobulin light chain** -binding **domain** of **protein L**.
AU Wikstrom M.; **Sjobring U.**; Kastern W.; **Bjorck L.**; Drakenberg T.; Forsen S.
CS Physical Chemistry 2, Chemical Center, P.O. Box 124,S-221 00 Lund, Sweden
SO Biochemistry, (1993) 32/13 (3381-3386).
ISSN: 0006-2960 CODEN: BICHAW
CY United States
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LA English
SL English
AB The 1H NMR assignments have been made for the **immunoglobulin** (Ig) **light chain**-binding B1 **domain** of **protein L** from Peptostreptococcus magnus. The secondary structure elements and the global folding pattern were determined from nuclear Overhauser effects, backbone coupling constants, and slowly exchanging amide protons. The B1 **domain** was found to be folded

into a globular unit of 61 amino acid residues, preceded by a 15 amino
acid long disordered N-terminus. The folded portion of the molecule
contains a four- stranded .beta.-sheet spanned by a central .alpha.-helix.
The fold is similar to the IgG-binding **domains** of streptococcal protein G, despite the fact that the binding sites on **immunoglobulin** for the two proteins are different; protein G binds
IgG through the constant (Fc) part of the heavy chain, whereas **protein L** has affinity for the variable **domain** of Ig light chains.

L7 ANSWER 20 OF 24 BIOSIS COPYRIGHT 2002 BIOSIS
AN 1993:242227 BIOSIS
DN PREV199344115427
TI NMR studies of an **immunoglobulin light chain** -binding **protein L domain**.
AU Wikstrom, Mats (1); **Sjobring, Ulf**; Kastern, William; **Bjorck, Lars**; Drakenberg, Torbjorn; Forsen, Sture
CS (1) Dep. Physical Chem., Univ. Lund, Lund Sweden
SO Journal of Cellular Biochemistry Supplement, (1993) Vol. 0, No. 17 PART C,
pp. 304.
Meeting Info.: Keystone Symposium on Frontiers of NMR in Molecular Biology
III Taos, New Mexico, USA March 8-14, 1993
ISSN: 0733-1959.
DT Conference
LA English

L7 ANSWER 21 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 15
AN 93269935 EMBASE
DN 1993269935
TI Purification of antibodies using **protein L**-binding framework structures in the **light chain** variable **domain**.
AU Nilson B.H.K.; Logdberg L.; Kastern W.; **Bjorck L.**; Akerstrom B.
CS Dept. of Medical/Physiol. Chemistry, University of Lund, P.O. Box 94,S-221
00 Lund, Sweden
SO Journal of Immunological Methods, (1993) 164/1 (33-40).
ISSN: 0022-1759 CODEN: JIMMBG
CY Netherlands
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
LA English
SL English
AB **Protein L** from the bacterial species Peptostreptococcus magnus binds specifically to the variable **domain** of Ig light chains, without interfering with the antigen-binding site. In this work a genetically engineered fragment of
protein L, including four of the repeated Ig-binding repeat units, was employed for the purification of Ig from various

sources. Thus, IgG, IgM, and IgA were purified from human and mouse serum in a single step using **protein L**-Sepharose affinity chromatography. Moreover, human and mouse monoclonal IgG, IgM, and IgA, and human IgG Fab fragments, as well as a mouse/human chimeric recombinant antibody, could be purified from cultures of hybridoma cells or antibody-producing bacterial cells, with **protein L** -Sepharose. This was also the case with a humanized mouse antibody, in which mouse hypervariable antigen-binding regions had been introduced into a **protein L**-binding .kappa. subtype III human IgG. These experiments demonstrate that it is possible to engineer antibodies and antibody fragments (Fab, Fv) with **protein L** -binding framework regions, which can then be utilized in a **protein L**-based purification protocol.

L7 ANSWER 22 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 16
AN 92243483 EMBASE
DN 1992243483
TI Structure of peptostreptococcal **protein L** and identification of a repeated **immunoglobulin light chain**-binding **domain**.
AU Kastern W.; **Sjobring U.**; **Bjorck L.**
CS Department of Pathology, College of Medicine, University of Florida,Gainesville, FL 32610, United States
SO Journal of Biological Chemistry, (1992) 267/18 (12820-12825). ISSN: 0021-9258 CODEN: JBCHA3
CY United States
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
LA English
SL English
AB The gene for **protein L**, an **immunoglobulin** (Ig) **light chain**-binding protein expressed by some strains of the anaerobic bacterial species Peptostreptococcus magnus, was cloned and sequenced. The gene translates into a protein of 719 amino acid residues. Following a signal sequence of 18 amino acids and a NH2-terminal region ('A') of 79 residues, the molecule contains five homologous 'B' repeats of 72-76 amino acids each. Further, toward the COOH terminus, two additional repeats ('C') were found. These are not related to the 'B' repeats, but are highly homologous to each other. After the C repeats (52 amino acids each), a hydrophilic, proline-rich putative cell wall-spanning region ('W') was found, followed at the COOH-terminal end by a hydrophobic membrane anchor ('M'). Fragments of the gene were expressed, and the

corresponding peptides were analyzed for Ig-binding activity. The B repeats were found to be responsible for the interaction with Ig light chains. An Escherichia coli high level expression system was adapted for the production of large amounts of two Ig-binding **protein L** fragments comprising one and four B repeats, respectively.

L7 ANSWER 23 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 17
AN 92311879 EMBASE
DN 1992311879
TI **Protein L** from Peptostreptococcus magnus binds to the .kappa. **light chain** variable **domain**.
AU Nilson B.H.K.; Solomon A.; **Bjorck L.**; Akerstrom B.
CS Medical/Physiological Chem. Dept., University of Lund, P. O. Box 94,S-221 00 Lund, Sweden
SO Journal of Biological Chemistry, (1992) 267/4 (2234-2239). ISSN: 0021-9258 CODEN: JBCHA3
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English
AB **Protein L** is an **immunoglobulin light chain**-binding protein expressed by some strains of the anaerobic bacterial species Peptostreptococcus magnus. The major variable region subgroups of human .kappa. and .lambda. light chains were tested for **protein L** binding; V(.kappa.I), V(.kappa.III), and V(.kappa.IV) bound **protein L**, whereas no binding occurred with proteins of the V(.kappa.II) subgroup or with any .lambda. **light chain** subgroups. Studies of the **protein L** binding capacity of naturally occurring V(L) fragments, and V(L)- and C(L)-related trypsin- and pepsin-derived peptides prepared from a .kappa.I **light chain**, localized the site of interaction to the V(L) **domain**. The affinity constant for the binding to an isolated V(.kappa.I) fragment was comparable to that for the native protein (K(.alpha.) 0.9 x 109 M-1 and K(.alpha.) 1.5 x 109 M-1, respectively). No binding occurred with C(L)-related fragments. Extensive reduction and alkylation of the V(.kappa.) fragment or the native .kappa. chain resulted in complete loss of **protein L** binding. Although it is possible, from comparative amino acid sequence data, to identify certain V(L)-framework region residues that account for the selective binding of **protein L** by .kappa.I, .kappa.III, and .kappa.IV proteins, our studies indicate that this interaction is essentially dependent upon the tertiary structural

integrity of the .kappa. chain V(L) **domain**.

L7 ANSWER 24 OF 24 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 18

AN 89281889 EMBASE
DN 1989281889
TI Ig-binding bacterial proteins also bind proteinase inhibitors.
AU **Sjobring U.**; Trojnar J.; Grubb A.; Akerstrom B.; **Bjorck L.**
CS Department of Medical Microbiology, University of Lund, 223 62 Lund, Sweden
SO Journal of Immunology, (1989) 143/9 (2948-2954).
ISSN: 0022-1767 CODEN: JOIMA3
CY United States
DT Journal
FS 004 Microbiology
026 Immunology, Serology and Transplantation
LA English
SL English
AB Protein G is a streptococcal cell wall protein with separate binding sites for IgG and human serum albumin (HSA). In the present work it was demonstrated that .alpha.2-macroglobulin (.alpha.2M) and kininogen, two proteinase inhibitors of human plasma, bound to protein G, whereas 23 other human proteins showed no affinity. .alpha.2M was found to interact with the IgG-binding **domains** of protein G, and in excess .alpha.2M inhibited IgG binding and vice versa. A synthetic peptide, corresponding to one of the homologous IgG-binding **domains** of protein G, blocked binding of protein G to .alpha.2M. Protein G showed affinity for both native and proteinase complexed .alpha.2M but did not bind to the reduced form of .alpha.2M, or to the C-terminal **domain** of the protein known to interact with .alpha.2M receptors on macrophages. Binding of protein G to .alpha.2M and kininogen did not interfere with their inhibitory activity on proteinases, and the interaction between protein G and the two proteinase inhibitors was not due to proteolytic activity of protein G. The finding that protein G has affinity for proteinase inhibitors was generalized to comprise also other Ig binding bacterial proteins. Thus, .alpha.2M and kininogen, were shown to bind both protein A of Staphylococcus aureus and **protein L** of Peptococcus magnus. The results described above suggest that Ig-binding proteins are involved in proteolytic events, which adds a new and perhaps functional aspect to these molecules.

```
=> s immunoglobulin? and (protein 1 or light chain or hybrid)

   6 FILES SEARCHED...
L8       39787 IMMUNOGLOBULIN? AND (PROTEIN L OR LIGHT CHAIN OR
HYBRID)

=> s l8 and domain?

L9        9085 L8 AND DOMAIN?

=> s l9 and immunoglobulin g

L10        850 L9 AND IMMUNOGLOBULIN G

=> s l10 and protein l

L11         42 L10 AND PROTEIN L

=> dup rem l11

PROCESSING COMPLETED FOR L11
L12          31 DUP REM L11 (11 DUPLICATES REMOVED)

=> d bib ab 1-31


L12  ANSWER 1 OF 31  USPATFULL
AN     2001:193946  USPATFULL
TI     Enhancement of antibody-mediated immune responses
IN     Ravetch, Jeffrey V., New York, NY, United States
PI     US 2001036459      A1   20011101
AI     US 2001-834321     A1   20010413 (9)
PRAI   US 2000-198550      20000413 (60)
       US 2000-204254      20000515 (60)
DT     Utility
FS     APPLICATION
LREP   Robin S, Quartin, Esq., Woodcock Washburn Kurtz, Mackiewicz &
Norris
       LLP, One Liberty Place-46th Floor, Philadelphia, PA, 19103
CLMN   Number of Claims: 21
ECL    Exemplary Claim: 1
DRWN   3 Drawing Page(s)
LN.CNT 1679
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The present invention is related to enhancing the function of
anti-tumor
       antibodies by regulating Fc.gamma.RIIB-mediated activity. In
particular,
       disrupting SHIP activation by Fc.gamma.RIIB enhances
cytotoxicity
       elicited by a therapeutic antibody in vivo in a human. The
invention
       further provides an antibody, e.g., an anti-tumor antibody,
with a
       variant Fc region that results in binding of the antibody to
       Fc.gamma.RIIB with reduced affinity. A variety of transgenic
mouse
```

models demonstrate that the inhibiting Fc.gamma.RIIB molecule is a potent regulator of cytotoxicity in vivo.

L12 ANSWER 2 OF 31 USPATFULL
AN 2001:36953 USPATFULL
TI Cytokine signal regulators
IN Yue, Henry, Sunnyvale, CA, United States
Corley, Neil C., Mountain View, CA, United States
Guegler, Karl J., Menlo Park, CA, United States
Baughn, Mariah R., San Leandro, CA, United States
PA Incyte Genomics, Inc., Palo Alto, CA, United States (U.S. corporation)
PI US 6201106 B1 20010313
AI US 1999-382086 19990824 (9)
RLI Division of Ser. No. US 1998-189035, filed on 10 Nov 1998, now patented,
Pat. No. US 6020165, issued on 1 Feb 2000
DT Utility
FS Granted
EXNAM Primary Examiner: Prouty, Rebecca E.; Assistant Examiner: Monshipouri,
Maryam
LREP Incyte Genomics, Inc.
CLMN Number of Claims: 4
ECL Exemplary Claim: 1
DRWN 15 Drawing Figure(s); 15 Drawing Page(s)
LN.CNT 2393
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides human cytokine signal regulators (CKSR) and
polynucleotides which identify and encode CKSR. The invention also
provides expression vectors, host cells, antibodies, agonists, and
antagonists. The invention also provides methods for diagnosing,
treating, or preventing disorders associated with expression of CKSR.

L12 ANSWER 3 OF 31 WPIDS COPYRIGHT 2002 DERWENT INFORMATION LTD
AN 2001-091926 [10] WPIDS
DNC C2001-027208
TI Recombinant respiratory syncytial virus (RSV) incorporating a heterologous
polynucleotide encoding an immune modulatory molecule is used as a vaccine
to provide an immune response to RSV.
DC B04 D16
IN BUKREYEV, A; COLLINS, P L; MURPHY, B R; WHITEHEAD, S S
PA (USSH) US DEPT HEALTH & HUMAN SERVICES
CYC 94
PI WO 2001004271 A2 20010118 (200110)* EN 154p
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ
NL OA PT SD SE SL SZ TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM
DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC

LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE
SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
AU 2000062112 A 20010130 (200127)
ADT WO 2001004271 A2 WO 2000-US19042 20000712; AU 2000062112 A AU 2000-62112
20000712
FDT AU 2000062112 A Based on WO 200104271
PRAI US 1999-143425P 19990713
AB WO 200104271 A UPAB: 20010220
NOVELTY - Infectious recombinant respiratory syncytial virus (RSV) (I)
comprising a recombinant RSV genome or antigenome incorporating a heterologous polynucleotide encoding an immune modulatory molecule, a
major nucleocapsid (N) protein, nucleocapsid phosphoprotein (P), large
polymerase **protein** (L) and a RNA polymerase elongation
factor, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the
following:
(1) an isolated polynucleotide molecule (II) comprising a RSV genome
or antigenome modified to incorporate a polynucleotide sequence encoding
an immune modulatory molecule; and
(2) a method for producing an infectious attenuated RSV particle from
one or more isolated polynucleotide molecules encoding the RSV.
ACTIVITY - Immunostimulator.
Balb/c mice were infected intranasally with 106 plaque forming units
(pfu) rRSV/mIFN gamma , rRSV/chloramphenicol acetyl transferase (CAT) or
wt RSV. Serum samples were collected on days 0, 28 and 56 and analyzed by
RSV-specific and antibody isotype-specific enzyme linked immunosorbent
assay and by an RSV neutralization assay. The levels of IgA antibodies
induced by the viruses were not significantly different, there was a
significant increase, four fold, in total IgG specific to RSV F protein in
mice vaccinated with rRSV/mIFN gamma compared to animals vaccinated with
wt RSV or RSV/CAT on day 56 but not on day 28. Neutralizing antibody
titers of mice infected with rRSV/mIFN gamma compared with wt RSV and
RSV/CAT were lower on day 28 but modestly higher on day 56.
MECHANISM OF ACTION - Vaccine.
USE - (I) elicits a protective immune response to RSV in a vaccinated
host (claimed). (I) is administered to an individual seronegative for
antibodies to RSV or possessing transplacentally acquired maternal

antibodies to RSV. (I) elicits an immune response against human RSV A
and/or RSV B.
ADVANTAGE - (I) induces titers of serum **Immunoglobulin G** (IgG) that are at least 2-10 fold higher than levels of serum IgG induced by wt RSV.
Previously a chemotherapeutic agent ribavirin and pooled donor IgG
has been used to treat RSV but these methods lack long-term effectiveness
and are inappropriate for widespread use.
Dwg.0/7

L12 ANSWER 4 OF 31 BIOSIS COPYRIGHT 2002 BIOSIS
AN 2001:261065 BIOSIS
DN PREV200100261065
TI Structures of the B1 **domain** of **protein L**
from Peptostreptococcus magnus with a tyrosine to tryptophan substitution.
AU O'Neill, Jason W.; Kim, David E.; Baker, David; Zhang, Kam Y. J. (1)
CS (1) Division of Basic Sciences, Fred Hutchinson Cancer Research Center,
1100 Fairview Avenue North, Seattle, WA, 98109: kzhang@fhcrc.org USA
SO Acta Crystallographica Section D Biological Crystallography, (April, 2001)
Vol. 57, No. 4, pp. 480-487. print.
ISSN: 0907-4449.
DT Article
LA English
SL English
AB The three-dimensional structure of a tryptophan-containing variant of the
IgG-binding B1 **domain** of **protein L** has been
solved in two crystal forms to 1.7 and 1.8 ANG resolution. In one of the
crystal forms, the entire N-terminal histidine-tag region was immobilized
through the coordination of zinc ions and its structural conformation
along with the zinc coordination scheme were determined. However, the
ordering of the histidine tag by zinc does not affect the overall
structure of the rest of the protein. Structural comparisons of the
tryptophan-containing variant with an NMR-derived wild-type structure,
which contains a tyrosine at position 47, reveals a common fold, although
the overall backbone root-mean-square difference is 1.5 ANG. The Y47W
substitution only caused local rearrangement of several side chains, the
most prominent of which is the rotation of the Tyr34 side chain, resulting
in a 6 ANG displacement of its hydroxyl group. A small methyl-sized cavity
bounded by beta-strands 1, 2 and 4 and the alpha-helix was found in the

structures of the Y47W-substituted **protein L** B1 **domain**. This cavity may be created as the result of subsequent side-chain rearrangements caused by the Y47W substitution. These high-resolution structures of the tryptophan-containing variant provide a reference frame for the analysis of thermodynamic and kinetic data derived from a series of mutational studies of the **protein L** B1 **domain**.

L12 ANSWER 5 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 1
AN 2001037308 EMBASE
TI Studies on a single **immunoglobulin**-binding **domain** of **protein L** from Peptostreptococcus magnus: The role of tyrosine-53 in the reaction with human IgG.
AU Beckingham J.A.; Housden N.G.; Muir N.M.; Bottomley S.P.; Gore M.G.
CS M.G. Gore, Div. of Biochemistry/Molecular Biol., School of Biological Sciences, University of Southampton, Bassett Crescent East, Southampton, Hants. S016 7PX, United Kingdom. m.g.gore@soton.ac.uk
SO Biochemical Journal, (15 Jan 2001) 353/2 (395-401).
Refs: 24
ISSN: 0264-6021 CODEN: BIJOAK
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
LA English
SL English
AB Chemical modification experiments with tetranitromethane (TNM) have been used to investigate the role of tyrosine residues in the formation of the complex between PpL (the single Ig-binding **domain** of **protein L**, isolated from P. magnus strain 3316) and the kappa **light chain** (.kappa.-chain). Reaction of PpL with TNM causes the modification of 1.9 equiv. of tyrosine (Tyr(51) and Tyr(53)) and results in an approx. 140-fold decrease in affinity for human IgG. Similar experiments with mutated PpL proteins suggest that nitration predominantly inactivates the protein by modification of Tyr(53). Reduction of the nitrotyrosine groups to aminotyrosine by incubation with sodium hydrosulphite does not restore high affinity for IgG. Modification of .kappa.-chain by TNM resulted in the nitration of 3.1.+-.0.09 tyrosine residues. When the PpL-.kappa.-chain complex was incubated with TNM, 4.1.+-.0.04 tyrosine residues were nitrated, indicating that one tyrosine residue previously modified by the reagent was protected from TNM when the proteins are in complex with each other. The K(d) for the equilibrium

between PpL, human IgG and their complex has been shown by ELISA to be 112
.+-. 20 nM. A similar value (153.+-.33nM) was obtained for the complex
formed between IgG and the Tyr(64) .fwdarw. Trp mutant (Y64W). However,
the K(d) values for the equilibria involving the PpL mutants Y53F and
Y53F,Y64W were found to be 3.2.+-.0.2 and 4.6.+-.1 .mu.M respectively.
These suggest that the phenol group of Tyr(53) in PpL is important to the
stability of the PpL-.kappa.-chain complex.

L12 ANSWER 6 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 2
AN 2001104980 EMBASE
TI A "loop entropy reduction" phage-display selection for folded amino acid
sequences.
AU Minard P.; Scalley-Kim M.; Watters A.; Baker D.
CS D. Baker, Department of Biochemistry, University or Washington, J 567
Health Sciences Building, Box 37-7350, Seattle, WA 98195, United States.
dabaker@u.washington.edu
SO Protein Science, (2001) 10/1 (129-134).
Refs: 25
ISSN: 0961-8368 CODEN: PRCIEI
CY United States
DT Journal; Article
FS 022 Human Genetics
029 Clinical Biochemistry
LA English
SL English
AB As a step toward selecting folded proteins from libraries of randomized
sequences, we have designed a 'loop entropy reduction'-based phage-display
method. The basic premise is that insertion of a long disordered sequence
into a loop of a host protein will substantially destabilize the host
because of the entropic cost of closing a loop in a disordered chain. If
the inserted sequence spontaneously folds into a stable structure with the
N and C termini close in space, however, this entropic cost is diminished.
The host protein function can, therefore, be used to select folded
inserted sequences without relying on specific properties of the inserted
sequence. This principle is tested using the IgG binding **domain** of **protein** **L** and the 1ck SH2 **domain** as host
proteins. The results indicate that the loop entropy reduction screen is
capable of discriminating folded from unfolded sequences when the proper

host protein and insertion point are chosen.

L12 ANSWER 7 OF 31 BIOSIS COPYRIGHT 2002 BIOSIS
AN 2001:243717 BIOSIS
DN PREV200100243717
TI The role of tyrosine residues of **protein L** in the binding reaction with human IgG.
AU Housden, N. G. (1); Beckingham, J. A. (1); Muir, N. M. (1); Bottomley, S. P. (1); Gore, M. G. (1)
CS (1) Institute of Biomolecular Sciences, University of Southampton, Bassett Crescent East, Southampton, SO16 7PX UK
SO Biochemical Society Transactions, (2001) Vol. 29, No. 1, pp. A22. print.
Meeting Info.: 672nd Meeting of the Biochemical Society Sussex, England, UK
ISSN: 0300-5127.
DT Conference
LA English
SL English

L12 ANSWER 8 OF 31 USPATFULL
AN 2000:138515 USPATFULL
TI Adsorbent for **immunoglobulins** and complexes thereof, adsorption method, and adsorption device
IN Yasuda, Takamune, Kobe, Japan
Odawara, Osamu, Takasago, Japan
Ogino, Eiji, Kobe, Japan
Nomura, Michio, Kakogawa, Japan
Nakai, Takahisa, Kobe, Japan
Asahi, Takashi, Kobe, Japan
Tani, Nobutaka, Osaka, Japan
PA Kaneka Corporation, Osaka, Japan (non-U.S. corporation)
PI US 6133431 20001017
WO 9726930 19970731
AI US 1998-117233 19981020 (9)
WO 1997-JP161 19970124
19981020 PCT 371 date
19981020 PCT 102(e) date
PRAI JP 1996-11281 19960125
DT Utility
FS Granted
EXNAM Primary Examiner: Saunders, David
LREP Fish & Neave, Haley, Jr., James F., Liang, Stanley D.
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 1489
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB An adsorbent that exhibits a high specificity in adsorbing **immunoglobulins** and/or complexes thereof, is extremely reduced in the lowering of the adsorption characteristic during sterilization or storage, is highly stable and safe, and is prepared by immobilizing on a water-insoluble support either a peptide derivative which has undergone

at least one of the deletion, substitution, insertion, or addition of amino acids in a peptide having a specified amino acid sequence or an amino acid sequence, or the above peptide derivative which has undergone the addition of Lyn or Cys at the amino and/or carboxyl terminal thereof; a device for adsorption and removal made by packing the adsorbent in a vessel equipped with effluent preventing means; and a method of adsorbing and removing **immunoglobulins** and/or complexes thereof contained in the blood, plasma or other body fluids with the adsorbent.

L12 ANSWER 9 OF 31 USPATFULL
AN 2000:80408 USPATFULL
TI Compositions for the prevention and treatment of verotoxin-induced disease
IN Williams, James A., Lincoln, NE, United States
Byrne, Lisa Marie, Stoughton, WI, United States
PA Ophidian Pharmaceuticals, Inc., Wisconsin, United States (U.S. corporation)
PI US 6080400 20000627
AI US 1997-816977 19970313 (8)
RLI Continuation-in-part of Ser. No. US 1995-410058, filed on 24 Mar 1995, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Housel, James C.; Assistant Examiner: Devi, S.
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 2
ECL Exemplary Claim: 1
DRWN 1 Drawing Figure(s); 9 Drawing Page(s)
LN.CNT 5468
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention includes methods for generating neutralizing antitoxin directed against verotoxins. In preferred embodiments, the antitoxin directed against these toxins is produced in avian species using soluble recombinant verotoxin proteins. This antitoxin is designed so as to be administrable in therapeutic amounts and may be in any form (i.e., as a solid or in aqueous solution). These antitoxins are useful in the treatment of humans and other animals intoxicated with at least one bacterial toxin, as well as for preventive treatment, and diagnostic assays to detect the presence of toxin in a sample.

L12 ANSWER 10 OF 31 USPATFULL
AN 2000:43944 USPATFULL
TI Purified and recombinant antigenic protein associated with abdominal aortic aneurysm (AAA) disease, and diagnostic and therapeutic use thereof
IN Tilson, Martin David, Scarsdale, NY, United States
PA The Trustees of Columbia University, New York, NY, United States (U.S. corporation)
PI US 6048704 20000411
AI US 1997-812586 19970307 (8)
PRAI US 1996-12976 19960307 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Housel, James C.; Assistant Examiner: Swartz, Rodney P.
LREP White, John P.Cooper & Dunham LLP
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 22 Drawing Figure(s); 24 Drawing Page(s)
LN.CNT 3522
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides an isolated protein of approximately 40 kDa which is purified from human aortic tissue and immunoreactive with AAA-associated **immunoglobulin**. Also provided are a method of diagnosing AAA disease in a subject using said isolated protein and a pharmaceutical composition comprising said isolated protein. A method of alleviating AAA disease in a subject comprising administering said pharmaceutical composition comprising the isolated protein is also provided. The subject invention also provides a recombinantly produced human aortic protein which is immunoreactive with AAA-associated **immunoglobulin**. Also provided are a method of diagnosing AAA disease in a subject using said recombinantly produced protein and a pharmaceutical composition comprising said recombinantly produced protein. A method of alleviating AAA disease in a subject comprising administering said pharmaceutical composition comprising the recombinantly produced protein is also provided.

L12 ANSWER 11 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 3
AN 2000328850 EMBASE
TI A breakdown of symmetry in the folding transition state of **protein L**.
AU Kim D.E.; Fisher C.; Baker D.

CS D. Baker, Department of Biochemistry, University of Washington, Seattle,
WA 98195, United States. dabaker@u.washington.edu
SO Journal of Molecular Biology, (19 May 2000) 298/5 (971-984).
Refs: 38
ISSN: 0022-2836 CODEN: JMOBAK
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
029 Clinical Biochemistry
LA English
SL English
AB The 62 residue IgG binding **domain** of **protein L**
consists of a central .alpha.-helix packed on a four-stranded .beta.-sheet
formed by N and C-terminal .beta.-hairpins. The overall topology of the
protein is quite symmetric: The .beta.-hairpins have similar lengths and
make very similar interactions with the central helix. Characterization of
the effects of 70 point mutations distributed throughout the protein on
the kinetics of folding and unfolding reveals that this symmetry is
completely broken during folding; the first .beta.-hairpin is largely
structured while the second .beta.-hairpin and helix are largely disrupted
in the folding transition state ensemble. The results are not consistent
with a 'hydrophobic core first' picture of protein folding; the first
.beta.-hairpin appears to be at least as ordered at the rate limiting step
in folding as the hydrophobic core. (C) 2000 Academic Press.

L12 ANSWER 12 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 2000290145 EMBASE
TI Critical role of .beta.-hairpin formation in protein G folding.
AU McCallister E.L.; Alm E.; Baker D.
CS D. Baker, Department of Biochemistry, University of Washington, Seattle,
WA 98195, United States. dabaker@u.washington.edu
SO Nature Structural Biology, (2000) 7/8 (669-673).
ISSN: 1072-8368 CODEN: NSBIEW
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English
AB Comparison of the folding mechanisms of proteins with similar structures
but very different sequences can provide fundamental insights into the
determinants of protein folding mechanisms. Despite very little sequence
similarity, the .apprx.60 residue IgG binding **domains** of protein
G and **protein L** both consist of a single helix packed

against a four-stranded sheet formed by two symmetrically disposed .beta.-hairpins. We demonstrate that, as in the case of **protein L**, one of the two .beta.-turns of protein G is formed and the other disrupted in the folding transition state. Unlike **protein L**, however, in protein G it is the second .beta.-turn that is formed in the folding transition state ensemble. Substitution of an Asp residue by Ala in protein G that eliminates an i,i+2 side chain-main chain hydrogen bond in the second .beta.-turn slows the folding rate .apprx.20-fold but has virtually no effect on the unfolding rate. Taken together with previous results, these findings suggest that the presence of an intact .beta.-turn in the folding transition state is a consequence of the overall topology of **protein L** and protein G, but the particular hairpin that is formed is determined by the detailed interatomic interactions that determine the free energies of formation of the isolated .beta.-hairpins.

L12 ANSWER 13 OF 31 USPATFULL
AN 1999:124726 USPATFULL
TI **Protein L** and **hybrid** proteins thereof
IN Bjorck, Lars, Sodra Sandby, Sweden
Sjobring, Ulf, Lund, Sweden
PA Actinova Ltd., Lund, Sweden (non-U.S. corporation)
PI US 5965390 19991012
AI US 1997-795475 19970211 (8)
RLI Division of Ser. No. US 1994-325278, filed on 26 Oct 1994
PRAI SE 1992-1331 19920428
DT Utility
FS Granted
EXNAM Primary Examiner: Degen, Nancy
LREP Seed and Berry LLP
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN 17 Drawing Figure(s); 17 Drawing Page(s)
LN.CNT 1305
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to sequences of **protein L** which bind to light chains of **immunoglobulins**. The invention also relates to **hybrid** proteins thereof which are able to bind to both light and heavy chains of **immunoglobulin G**, in particular protein LG. The invention also relates to DNA-sequences which code for the proteins, vectors which include such DNA-sequences, host cells which have been transformed with the vectors, methods for producing the proteins, reagent appliances for separation and identification of **immunoglobulins**, compositions and pharmaceutical compositions and pharmaceutical compositions which contain the proteins.

L12 ANSWER 14 OF 31 USPATFULL
AN 1999:18714 USPATFULL
TI Gene therapy methods and compositions
IN Oin, Xiao-Oiang, Brighton, MA, United States
PA Biogen, Inc, Cambridge, MA, United States (U.S. corporation)
PI US 5869040 19990209
AI US 1995-481814 19950607 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Yucel, Irem
LREP Biogen, Inc., Kaplan, Warren A.
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN 2 Drawing Figure(s); 2 Drawing Page(s)
LN.CNT 2515
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to uses of mutant proto-oncogenes and oncoproteins expressed by the proto-oncogenes in inhibiting tumor growth and/or inhibiting the transformed phenotype. The preferred oncoprotein is a dominant, interfering mutant of a nuclear E2F transcription factor protein and is preferably a mutant E2F1 transcription factor protein. Methods of treating a target cell are described. Treatment is accomplished by administering to a target cell a dominant interfering mutant of a proto-oncogene in an effective amount. Treatment is also accomplished by administering to a target cell an oncoprotein in an effective amount. Compositions for such use are described as well.

L12 ANSWER 15 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 2000005317 EMBASE
TI Robustness of protein folding kinetics to surface hydrophobic substitutions.
AU Gu H.; Doshi N.; Kim D.E.; Simons K.T.; Santiago J.V.; Nauli S.; Baker D.
CS D. Baker, Department of Biochemistry, University of Washington, Seattle, WA 98195, United States. dabaker@u.washington.edu
SO Protein Science, (1999) 8/12 (2734-2741).
Refs: 21
ISSN: 0961-8368 CODEN: PRCIEI
CY United States
DT Journal; Article
FS 004 Microbiology
LA English
SL English
AB We use both combinatorial and site-directed mutagenesis to explore the consequences of surface hydrophobic substitutions for the folding of two small single **domain** proteins, the src SH3 **domain**, and

the IgG binding **domain** of Peptostreptococcal **protein L**. We find that in almost every case, destabilizing surface hydrophobic substitutions have much larger effects on the rate of unfolding than on the rate of folding, suggesting that nonnative hydrophobic interactions do not significantly interfere with the rate of core assembly.

L12 ANSWER 16 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 1999191641 EMBASE
TI Chain collapse can occur concomitantly with the rate-limiting step in protein folding.
AU Plaxco K.W.; Millett I.S.; Segel D.J.; Doniach S.; Baker D.
CS D. Baker, Department of Biochemistry, University of Washington, Seattle, WA 98195, United States. dabaker@u.washington.edu
SO Nature Structural Biology, (1999) 6/6 (554-556).
Refs: 26
ISSN: 1072-8368 CODEN: NSBIEW
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English
AB We have directly characterized the extent of chain collapse early in the folding of **protein L** using time-resolved small angle X-ray scattering. We find that, immediately after the initiation of refolding, the protein exhibits dimensions indistinguishable from those observed under highly denaturing, equilibrium conditions and that this expanded initial state collapses with the same rate as that of the overall folding reaction. The observation that chain compaction need not significantly precede the rate- limiting step of folding demonstrates that rapid chain collapse is not an obligatory feature of protein folding reactions.

L12 ANSWER 17 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 4
AN 1998388402 EMBASE
TI Limited internal friction in the rate-limiting step of a two-state protein folding reaction.
AU Plaxco K.W.; Baker D.
CS D. Baker, Department of Biochemistry, Box 357350, University of Washington, Seattle, WA 98195-7350, United States. baker@ben.bchem.washington.edu
SO Proceedings of the National Academy of Sciences of the United States of America, (10 Nov 1998) 95/23 (13591-13596).
Refs: 35
ISSN: 0027-8424 CODEN: PNASA6
CY United States

DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English
AB Small, single-**domain** proteins typically fold via a compact transition- state ensemble in a process well fitted by a simple, two-state model. To characterize the rate-limiting conformational changes that underlie two- state folding, we have investigated experimentally the effects of changing solvent viscosity on the refolding of the IgG binding **domain** of **protein L**. In conjunction with numerical simulations, our results indicate that the rate-limiting conformational changes of the folding of this **domain** are strongly coupled to solvent viscosity and lack any significant 'internal friction' arising from intrachain collisions. When compared with the previously determined solvent viscosity dependencies of other, more restricted conformational changes, our results suggest that the rate-limiting folding transition involves conformational fluctuations that displace considerable amounts of solvent. Reconciling evidence that the folding transition state ensemble is comprised of highly collapsed species with these and similar, previously reported results should provide a significant constraint for theoretical models of the folding process.

L12 ANSWER 18 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 5
AN 1998416862 EMBASE
TI Protein LA, a novel **hybrid** protein with unique single-chain Fv antibody- and Fab-binding properties.
AU Svensson H.G.; Hoogenboom H.R.; Sjobring U.
CS U. Sjobring, Department of Medical Microbiology, Solvegatan 23, S-22362 Lund, Sweden. ulf.sjobring@mmb.lu.se
SO European Journal of Biochemistry, (1 Dec 1998) 258/2 (890-896). Refs: 44
ISSN: 0014-2956 CODEN: EJBCAI
CY United Kingdom
DT Journal; Article
FS 026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LA English
SL English
AB Existing Ig-binding proteins all suffer from limitations in their binding spectrum. In the pursuit of the ultimate, non-restricted, Ig-binding protein, we have constructed the **hybrid** protein LA, by fusing four of the Ig.kappa. **light-chain**-binding

domains of peptostreptococcal **protein L** with four of the IgGFc- and Fab-binding regions of staphylococcal protein A. Ligand-blot experiments demonstrated that the L and the A components were both functional in the **hybrid**, as the protein was shown to bind purified x light chains and IgGFc. Protein LA bound human Ig of different classes and IgG from a wide range of mammalian species. IgG, IgM and IgA were purified from human serum and saliva by affinity chromatography on protein LA agarose. Similarly, single-chain Fv (scFv) antibodies carrying the .kappa. **light-chain** variable **domain** or expressing the V(H)III (variable **domain** of the heavy chain of Ig) determinant, were efficiently purified on immobilized protein LA. As judged by surface plasmon resonance (SPR), protein LA showed enhanced affinity for all tested ligands, including several scFv antibodies, compared with proteins L and A alone. SPR analysis also demonstrated that binding of a ligand to one of the components in protein LA did not affect the ability of the **hybrid** protein to interact simultaneously with a ligand for the other component. The antigen-binding capacity of a .kappa.-expressing scFv antibody was unaffected by the interaction with protein LA, whereas the binding of a V(H)III-expressing scFv antibody to its antigen was, unexpectedly, blocked by protein A and protein LA. Together, these data demonstrate that protein LA represents a highly versatile Ig-binding molecule.

L12 ANSWER 19 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 6
AN 97098945 EMBASE
DN 1997098945
TI Kinetics of folding of the IgG binding **domain** of peptostreptoccocal **protein L**.
AU Scalley M.L.; Yi Q.; Gu H.; McCormack A.; Yates III J.R.; Baker D.
CS D. Baker, Department of Biochemistry, University of Washington, Seattle, WA 98195, United States
SO Biochemistry, (1997) 36/11 (3373-3382).
Refs: 38
ISSN: 0006-2960 CODEN: BICHAW
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English
AB The kinetics of folding of a tryptophan containing mutant of the IgG

binding **domain** of **protein L** were characterized using stopped-flow circular dichroism, stopped-flow fluorescence, and HD exchange coupled with high- resolution mass spectrometry. Both the thermodynamics and kinetics of folding fit well to a simple two-state model: (1) Guanidine induced equilibrium denaturation transitions measured by fluorescence and circular dichroism were virtually superimposable. (2) The kinetics of folding/unfolding were single exponential under all conditions examined, and the rate constants obtained using all probes were similar. (3) Mass spectra from pulsed HD exchange refolding experiments showed that a species with very little protection from exchange is converted to a fully protected species (the native state) at a rate very similar to that of the overall change in tryptophan fluorescence; no intervening partially protected species were observed. (4) Rate constants (in H2O) and m values for folding and unfolding determined by fitting observed relaxation rates obtained over a broad range of denaturant concentrations to a two-state model were consistent with the equilibrium parameters .DELTA.G and m: -RT In(k(u)/k(f))/.DELTA.G(U)(H2O) = 1.02; (m(u) + m(f))/m = 1.08. In contrast to results with a number of other proteins, there was no deviation from linearity in plots of In k(obs) versus guanidine at low guanidine concentrations, both in the presence and absence of 0.4 M Na2SO4, suggesting that significantly stabilized intermediates do not accumulate during folding. Although all of the change in fluorescence signal during folding in phosphate buffer was accounted for by the simple exponential describing the overall folding reaction, fluorescence-quenching experiments using sodium iodide revealed a small reduction in the extent of quenching of the protein within the first two milliseconds after initiation of refolding in low concentrations of guanidine, suggesting a partial collapse of the unfolded chain may occur under these conditions. Comparison with results on the structurally and functionally similar IgG binding **domain** of streptococcal protein G show intriguing differences in the folding of the two proteins.

L12 ANSWER 20 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 7
AN 96178843 EMBASE
DN 1996178843

TI Direct evidence for a two-state protein unfolding transition from hydrogen-deuterium exchange, mass spectrometry, and NMR.
AU Yi Q.; Baker D.
CS Department of Biochemistry, University of Washington,Seattle, WA 98195,
United States
SO Protein Science, (1996) 5/6 (1060-1066).
ISSN: 0961-8368 CODEN: PRCIEI
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English
AB We use mass spectrometry in conjunction with hydrogen-deuterium exchange
and NMR to characterize the conformational dynamics of the 62-residue IgG
binding **domain** of **protein L** under conditions
in which the native state is marginally stable. Mass spectra of **protein L** after short incubations in D2O reveal the
presence of two distinct populations containing different numbers of
protected protons. NMR experiments indicate that protons in the hydrophobic core are protected in one population, whereas all protons are
exchanged for deuterons in the other. As the exchange period is increased,
molecules are transferred from the former population to the latter. The
absence of molecules with a subset of the core protons protected suggests
that exchange occurs in part via a highly concerted transition to an
excited state in which all protons exchange rapidly with deuterons. A
steady increase in the molecular weight of the population with protected
protons, and variation in the exchange rates of the individual protected
protons indicates the presence of an additional exchange mechanism. A
simple model in which exchange results from rapid (> 105/s) local fluctuations around the native state superimposed upon transitions to an
unfolded excited state at .apprx.0.06/s is supported by qualitative
agreement between the observed mass spectra and the mass spectra simulated
according to the model using NMR-derived estimates of the proton exchange
rates.

L12 ANSWER 21 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 8
AN 96295065 EMBASE
DN 1996295065
TI Characterization of the binding properties of protein LG, an **immunoglobulin**-binding **hybrid** protein.
AU Kihlberg B.-M.; Sjoholm A.G.; Bjorck L.; Sjobring U.

CS Department of Medical Microbiology, Lund University,S-223 62 Lund, Sweden
SO European Journal of Biochemistry, (1996) 240/3 (556-563).
ISSN: 0014-2956 CODEN: EJBCAI
CY Germany
DT Journal; Article
FS 026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LA English
SL English
AB Protein LG is a 50-kDa **hybrid** molecule containing four Ig-**light-chain**-binding **domains** from **protein L** of Peptostreptococcus magnus and two IgG-Fc binding repeats from streptococcal protein G. Here we analyse the binding of protein LG to Ig from several mammalian species. Protein LG was shown to bind human IgG of all subclasses and other Ig classes that carry K chains. The binding to human IgG was only marginally influenced by changes in temperature (4-37.degree.C) or salt concentration (0-1.6 M), and was stable over a wide pH range (pH 4-10). Protein LG bound to Ig from 11 of 12 mammalian species, including those of rabbit, mouse and rat. The affinity constants obtained for the interactions between protein LG and polyclonal IgG from rabbit (4.0 x 109 M-1), mouse (1.7 x 109 M-1) and rat (1.3 X 109 M-1) were similar to the value previously reported for the interaction between the **hybrid** protein and human polyclonal IgG (5.9 x 109M-1. The interaction between protein LG and a mouse IgG mAb was not infuenced by the presence of the specific protein antigen, nor was the binding of this antibody to its ligand affected by protein LG. Inhibition experiments demonstrated that the Ig-binding site of one of the fusion partners retained its ligand-binding capacity when the other component was occupied. Protein LG selectively absorbed 85-90% of the total Ig present in human and rabbit sera and 75-80% of the Ig in sera from mouse and rat. Human serum depleted of C1q, factor D and properdin and preabsorbed by protein LG could be used as a source for other complement factors. These data demonstrate that protein LG is a very versatile Ig-binding protein.

L12 ANSWER 22 OF 31 BIOSIS COPYRIGHT 2002 BIOSIS
AN 1996:117934 BIOSIS
DN PREV199698690069
TI Backbone dynamics of a **domain** of **protein L**

which binds to **immunoglobulin** light chains.
AU Wikstrom, Mats (1); Forsen, Sture; Drakenberg, Torbjorn
CS (1) Physical Chem. 2, Chem. Cent., P.O. Box 121, S-221 00 Lund Sweden
SO European Journal of Biochemistry, (1996) Vol. 235, No. 3, pp. 543-548.
ISSN: 0014-2956.
DT Article
LA English
AB **Protein L** is a multidomain protein expressed at the surface of some strains of the anaerobic bacterial species Peptostreptococcus magnus. The molecule interacts with the variable **domain** of **immunoglobulin** (Ig) light chains through five repeated homologous **domains** denoted B1 to B5. The fold of the Ig-**light-chain**-binding B1 **domain** of **protein L** (PLB1) has been shown to comprise an alpha-helix packed against a four-stranded beta-sheet and therefore resembles the structure of the IgG-binding **domains** of streptococcal protein G. In the present study, amide-proton exchange and 15N-relaxation NMR measurements were performed on the B1 **domain** to investigate its backbone mobility. It was shown that the folded portion of PLB1 is rigid with no regions of significantly higher flexibility than average. The N-terminus, however, is highly flexible consistent with earlier studies on the solution structure of PLB1. Comparison of the amide-proton-exchange data with similar measurements performed on the IgG-binding **domains** of protein G indicates that the two proteins have different exchange behaviors in their second beta-strands. Both protein G and L employ this region of their structures for binding to **immunoglobulins** since the interaction of protein G and **protein L** with IgG Fab and the Ig **light chain**, respectively, involves residues from the second beta-strand.

L12 ANSWER 23 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 95191451 EMBASE
DN 1995191451
TI A phage display system for studying the sequence determinants of protein folding.
AU Gu H.; Yi Q.; Bray S.T.; Riddle D.S.; Shiau A.K.; Baker D.
CS Department of Biochemistry, University of Washington,Seattle, WA 98195, United States
SO Protein Science, (1995) 4/6 (1108-1117).
ISSN: 0961-8368 CODEN: PRCIEI
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English

SL English
AB We have developed a phage display system that provides a means to select variants of the IgG binding **domain** of peptostreptococcal **protein L** that fold from large combinatorial libraries. The premise underlying the selection scheme is that binding of **protein L** to IgG requires that the protein be properly folded. Using a combination of molecular biological and biophysical methods, we show that this assumption is valid. First, the phage selection procedure strongly selects against a point mutation in **protein L** that disrupts folding but is not in the IgG binding interface. Second, variants recovered from a library in which the first third of **protein L** was randomized are properly folded. The degree of sequence variation in the selected population is striking: the variants have as many as nine substitutions in the 14 residues that were mutagenized. The approach provides a selection for 'foldedness' that is potentially applicable to any small binding protein.

L12 ANSWER 24 OF 31 JICST-EPlus COPYRIGHT 2002 JST
AN 950744862 JICST-EPlus
TI High Level Expression of **Protein L**, an **Immunoglobulin**-Binding Protein, in Escherichia coli.
AU TOCAJ A; SJOEBRING U; BJOERCK L; HOLST O
CS Lund Univ., Lund, SWE
SO J Ferment Bioeng, (1995) vol. 80, no. 1, pp. 1-5. Journal Code: G0535B
(Fig. 2, Tbl. 1, Ref. 20)
CODEN: JFBIEX; ISSN: 0922-338X
CY Japan
DT Journal; Article
LA English
STA New
AB A high level expression system for production of an **immunoglobulin**-binding protein, in Escherichia coli was studied. The protein, called protein LI-IV, consists of four **immunoglobulin**-binding **domains** of the native **protein L**. A simple fed-batch cultivation strategy was used to investigate the influence of different induction times on cell growth, viability, acetic acid formation and product formation. Induction allowing product formation for several hours, i.e., in this case in early exponential phase, was most favorable in terms of product yields. The highest specific yield obtained was 150 mg protein per gram cell dry weight (dw), corresponding to 360 mg per liter broth. The leakage of product into the media was less than 5%. Induction in early exponential phase lead to the highest amount of acetic acid, 1.47

g/g dw. Viability decreased significantly after induction. (author abst.)

L12 ANSWER 25 OF 31 BIOSIS COPYRIGHT 2002 BIOSIS
AN 1995:68832 BIOSIS
DN PREV199598083132
TI Three-dimensional solution structure of an **immunoglobulin light chain**-binding **domain** of **protein L**. comparison with the IgG-binding **domains** of protein G.
AU Wikstrom, Mats (1); Drakenberg, Torbjorn; Forsen, Sture; Sjobring, Ulf; Bjorck, Lars
CS (1) Dep. Physical Chem. 2, Medical Microbiol., Lund University, Lund Sweden
SO Biochemistry, (1994) Vol. 33, No. 47, pp. 14011-14017. ISSN: 0006-2960.
DT Article
LA English
AB **Protein L** is a multidomain protein expressed at the surface of some strains of the anaerobic bacterial species Peptostreptococcus magnus. It has affinity for **immunoglobulin** (Ig) through interaction with framework structures in the variable Ig **light chain domain**. The Ig-binding activity is located to five homologous repeats called B1-B5 in the N-terminal part of the protein. We have determined the three-dimensional solution structure of the 76 amino acid residue long B1 **domain** using NMR spectroscopy and distance geometry-restrained simulated annealing. The **domain** is composed of a 15 amino acid residue long disordered N-terminus followed by a folded portion comprising an alpha-helix packed against a four-stranded beta-sheet. These secondary structural elements are well determined with a backbone atomic root mean square deviation from their mean of 0.54 ANG . The B **domains** of **protein L** show very limited sequence homology to the **domains** of streptococcal protein G interacting with the heavy chains of IgG. However, despite this fact, and their different binding properties, the fold of the B1 **domain** was found to be similar to the fold of the IgG-binding protein G **domains** (Wikstrom, M., Sjobring, U., Kastem, W., Bjorck, L., Drakenberg, T., & Forsen, S. (1993) Biochemistry 32, 3381-3386). In the present study, the solution structure of the B1 **domain** enabled a more detailed comparison which can explain the different Ig-binding specificities of these two bacterial surface proteins. Among the differences observed, the alpha-helix orientation is the most striking. Thus, in the B1 **domain** of **protein L** the helix is almost parallel to the beta-sheet, whereas in the protein G **domains** the helix runs diagonally across the sheet.

L12 ANSWER 26 OF 31 BIOSIS COPYRIGHT 2002 BIOSIS

AN 1994:346388 BIOSIS
DN PREV199497359388
TI **Immunoglobulin** Fab fragment-binding proteins.
AU Bouvet, Jean-Pierre
CS Unite d'Immunologie Microbienne, Inst. Pasteur, 25 rue Dr Roux, F-75724
Paris 15 France
SO International Journal of Immunopharmacology, (1994) Vol. 16, No. 5-6, pp.
419-424.
ISSN: 0192-0561.
DT General Review
LA English
AB Five molecules are known to bind the Fab fragments of human **immunoglobulins** (Ig). Microbial protein A and protein G are primarily Fc-binding molecules but can also bind other structures of the heavy chain, which are located in the variable **domain** of the third subgroup (V-H3) and in the first constant **domain** of IgG (C-H1-r), respectively. In contrast, the two other microbial receptors have a sole Ig-binding site, directed to kappa chains (**protein L**) or to Ig polymers (protein P). Protein Fv is synthesized by human liver cells and released in the digestive lumen, where it forms large complexes with secretory Ig after binding to the VH **domains**. These five molecules, in the main, bind cleaved Ig and most of them recognize all classes of antibodies. Bacterial molecules are, or can be, used as reagents to purify and detect Ig and fragments. Furthermore, a possible use in human therapy or vaccination is envisaged, and the human protein Fv is a key-factor in immune protection against intraluminal pathogens of the gut.

L12 ANSWER 27 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 93126906 EMBASE
DN 1993126906
TI Proton nuclear magnetic resonance sequential assignments and secondary structure of an **immunoglobulin light chain** -binding **domain** of **protein L**.
AU Wikstrom M.; Sjobring U.; Kastern W.; Bjorck L.; Drakenberg T.; Forsen S.
CS Physical Chemistry 2, Chemical Center, P.O. Box 124,S-221 00 Lund, Sweden
SO Biochemistry, (1993) 32/13 (3381-3386).
ISSN: 0006-2960 CODEN: BICHAW
CY United States
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LA English
SL English
AB The 1H NMR assignments have been made for the **immunoglobulin**

(Ig) **light chain**-binding B1 **domain** of **protein L** from Peptostreptococcus magnus. The secondary structure elements and the global folding pattern were determined from nuclear Overhauser effects, backbone coupling constants, and slowly exchanging amide protons. The B1 **domain** was found to be folded into a globular unit of 61 amino acid residues, preceded by a 15 amino acid long disordered N-terminus. The folded portion of the molecule contains a four- stranded .beta.-sheet spanned by a central .alpha.-helix. The fold is similar to the IgG-binding **domains** of streptococcal protein G, despite the fact that the binding sites on **immunoglobulin** for the two proteins are different; protein G binds IgG through the constant (Fc) part of the heavy chain, whereas **protein L** has affinity for the variable **domain** of Ig light chains.

L12 ANSWER 28 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 9
AN 93269935 EMBASE
DN 1993269935
TI Purification of antibodies using **protein L**-binding framework structures in the **light chain** variable **domain**.
AU Nilson B.H.K.; Logdberg L.; Kastern W.; Bjorck L.; Akerstrom B.
CS Dept. of Medical/Physiol. Chemistry, University of Lund, P.O. Box 94,S-221 00 Lund, Sweden
SO Journal of Immunological Methods, (1993) 164/1 (33-40). ISSN: 0022-1759 CODEN: JIMMBG
CY Netherlands
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
LA English
SL English
AB **Protein L** from the bacterial species Peptostreptococcus magnus binds specifically to the variable **domain** of Ig light chains, without interfering with the antigen-binding site. In this work a genetically engineered fragment of **protein L**, including four of the repeated Ig-binding repeat units, was employed for the purification of Ig from various sources. Thus, IgG, IgM, and IgA were purified from human and mouse serum in a single step using **protein L**-Sepharose affinity chromatography. Moreover, human and mouse monoclonal IgG, IgM, and IgA, and human IgG Fab fragments, as well as a mouse/human chimeric recombinant antibody, could be purified from cultures of hybridoma cells or antibody-producing bacterial cells, with **protein L** -Sepharose. This was also the case with a humanized mouse antibody, in

which mouse hypervariable antigen-binding regions had been introduced into
a **protein L**-binding .kappa. subtype III human IgG.
These experiments demonstrate that it is possible to engineer antibodies
and antibody fragments (Fab, Fv) with **protein L**
-binding framework regions, which can then be utilized in a
protein L-based purification protocol.

L12 ANSWER 29 OF 31 BIOSIS COPYRIGHT 2002 BIOSIS
AN 1991:342266 BIOSIS
DN BA92:41641
TI EFFICIENT EXPRESSION OF A TRYPANOSOMA-CRUZI ANTIGEN IN ESCHERICHIA-COLI
AND STAPHYLOCOCCUS-AUREUS AND ITS RAPID PURIFICATION.
AU MORENO J I; SEIGELCHIFER M; ZORZOPULOS J
CS DEP. MOL. GENETICS, BIOSIDUS S.A., CONSTITUCION 4234, 1254 BUENOS AIRES,
ARGENTINA.
SO WORLD J MICROBIOL BIOTECHNOL, (1991) 7 (3), 316-323.
CODEN: WJMBEY. ISSN: 0959-3993.
FS BA; OLD
LA English
AB A Trypanosoma cruzi antigen gene was closed into a fusion vector based on
the IgG binding **domain** of Staphylococcus aureus protein A. This
vector transformed into Escherichia coli or Staphylococcus aureus and
produced about 12 mg fusion **protein/l** culture. In E.
coli, the product remained intracellular while in S. aureus it was
excreted into the growth medium. The **hybrid** protein was purified
by IgG Sepharose affinity chromatography. The presence of a cleavage site
for enterokinase between protein A and the T. cruzi antigen in the fusion
protein allowed the efficient release of the unfused antigen by enzymatic
treatment. Further affinity chromatography through IgG Sepharose resulted
in the production of the T. cruzi antigen free of protein A.

L12 ANSWER 30 OF 31 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 89281889 EMBASE
DN 1989281889
TI Ig-binding bacterial proteins also bind proteinase inhibitors.
AU Sjobring U.; Trojnar J.; Grubb A.; Akerstrom B.; Bjorck L.
CS Department of Medical Microbiology, University of Lund, 223 62 Lund,
Sweden
SO Journal of Immunology, (1989) 143/9 (2948-2954).
ISSN: 0022-1767 CODEN: JOIMA3
CY United States
DT Journal
FS 004 Microbiology
026 Immunology, Serology and Transplantation
LA English
SL English
AB Protein G is a streptococcal cell wall protein with separate binding sites

for IgG and human serum albumin (HSA). In the present work it was demonstrated that .alpha.2-macroglobulin (.alpha.2M) and kininogen, two proteinase inhibitors of human plasma, bound to protein G, whereas 23 other human proteins showed no affinity. .alpha.2M was found to interact with the IgG-binding **domains** of protein G, and in excess .alpha.2M inhibited IgG binding and vice versa. A synthetic peptide, corresponding to one of the homologous IgG-binding **domains** of protein G, blocked binding of protein G to .alpha.2M. Protein G showed affinity for both native and proteinase complexed .alpha.2M but did not bind to the reduced form of .alpha.2M, or to the C-terminal **domain** of the protein known to interact with .alpha.2M receptors on macrophages. Binding of protein G to .alpha.2M and kininogen did not interfere with their inhibitory activity on proteinases, and the interaction between protein G and the two proteinase inhibitors was not due to proteolytic activity of protein G. The finding that protein G has affinity for proteinase inhibitors was generalized to comprise also other Ig binding bacterial proteins. Thus, .alpha.2M and kininogen, were shown to bind both protein A of Staphylococcus aureus and **protein L** of Peptococcus magnus. The results described above suggest that Ig-binding proteins are involved in proteolytic events, which adds a new and perhaps functional aspect to these molecules.

L12 ANSWER 31 OF 31 LIFESCI COPYRIGHT 2002 CSA
AN 89:66455 LIFESCI
TI Ig-binding bacterial proteins also bind proteinase inhibitors.
AU Sjoebring, U.; Trojnar, J.; Grubb, A.; Aakerstroem, B.; Bjoerck, L.
CS Dep. Med. Microbiol., Soelvegatan 23, S-223 62 Lund, Sweden
SO J. IMMUNOL., (1989) vol. 143, no. 9, pp. 2948-2954.
DT Journal
FS J; F
LA English
SL English
AB Protein G is a streptococcal cell wall protein with separate binding sites for IgG and human serum albumin (HSA). In the present work it was demonstrated that alpha sub(2)-macroglobulin (alpha sub(2)M) and kininogen, two proteinase inhibitors of human plasma, bound to protein G, whereas 23 other human proteins showed no affinity. alpha sub(2)M was found to interact with the IgG-binding **domains** of protein G, and

in excess alpha sub(2)M inhibited IgG binding and vice versa. alpha
sub(2)M and kininogen were shown to bind both protein A of Staphylococcus
aureus) and **protein L** of Peptococcus magnus . The
results described above suggest that Ig-binding proteins are involved in
proteolytic events, which adds a new and perhaps functional aspect to
these molecules.

=> d his

(FILE 'HOME' ENTERED AT 15:58:56 ON 18 JAN 2002)

FILE 'EMBASE, MEDLINE, BIOSIS, USPATFULL, JAPIO, WPIDS, CAPLUS, AGRICOLA,
LIFESCI, BIOTECHDS, JICST-EPLUS' ENTERED AT 15:59:04 ON 18 JAN 2002

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                E BJORCK LARS/AU
L1          532 S E1-E4
                E SJOBRING ULF/AU
L2          151 S E2-E3
L3          614 S L1-L2
L4          233 S L3 AND IMMUNOGLOBULIN?
L5          102 S L4 AND (PROTEIN L OR LIGHT CHAIN OR HYBRID)
L6           62 S L5 AND DOMAIN?
L7           24 DUP REM L6 (38 DUPLICATES REMOVED)
L8        39787 S IMMUNOGLOBULIN? AND (PROTEIN L OR LIGHT CHAIN OR HYBRID)
L9         9085 S L8 AND DOMAIN?
L10         850 S L9 AND IMMUNOGLOBULIN G
L11          42 S L10 AND PROTEIN L
L12          31 DUP REM L11 (11 DUPLICATES REMOVED)
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=> s l10 and hybrid protein

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L13        143 L10 AND HYBRID PROTEIN
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=> dup rem l13

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PROCESSING COMPLETED FOR L13
L14         130 DUP REM L13 (13 DUPLICATES REMOVED)
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=> d bib 100-130

L14 ANSWER 100 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 95006043 EMBASE
DN 1995006043
TI Baculovirus-insect cell production of bioactive choriogonadotropin-
immunoglobulin G heavy-chain fusion proteins in sheep.
AU Johnson G.A.; Hansen T.R.; Austin K.J.; Van Kirk E.A.; Murdoch W.J.
CS Department of Animal Science, University of Wyoming,Laramie, WY 82071,

United States
SO Biology of Reproduction, (1995) 52/1 (68-73).
ISSN: 0006-3363 CODEN: BIREBV
CY United States
DT Journal; Article
FS 003 Endocrinology
026 Immunology, Serology and Transplantation
LA English
SL English

L14 ANSWER 101 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94366689 EMBASE
DN 1994366689
TI Regulation of p68 RNA helicase by calmodulin and protein kinase C.
AU Buelt M.K.; Glidden B.J.; Storm D.R.
CS Department of Pharmacology, University of Washington,Seattle, WA 98195,
United States
SO Journal of Biological Chemistry, (1994) 269/47 (29367-29370).
ISSN: 0021-9258 CODEN: JBCHA3
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
030 Pharmacology
037 Drug Literature Index
LA English
SL English

L14 ANSWER 102 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94306346 EMBASE
DN 1994306346
TI The disulfide linkages and glycosylation sites of the human natriuretic
peptide receptor-C homodimer.
AU Stults J.T.; O'Connell K.L.; Garcia C.; Wong S.; Engel A.M.; Garbers D.L.;
Lowe D.G.
CS Cardiovascular Research Department, Genentech, Inc.,South San Francisco,
CA 94080, United States
SO Biochemistry, (1994) 33/37 (11372-11381).
ISSN: 0006-2960 CODEN: BICHAW
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 103 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94186627 EMBASE
DN 1994186627
TI Expression and subcellular localization of poliovirus VPg-precursor
protein 3AB in eukaryotic cells: Evidence for glycosylation in vitro.
AU Datta U.; Dasgupta A.
CS Microbiology/Immunology Department, Jonsson Comprehensive Cancer Center,

University of California,Los Angeles, CA 90024-1747, United States
SO Journal of Virology, (1994) 68/7 (4468-4477).
ISSN: 0022-538X CODEN: JOVIAM
CY United States
DT Journal; Article
FS 004 Microbiology
LA English
SL English

L14 ANSWER 104 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94299231 EMBASE
DN 1994299231
TI Passive immunity to yersiniae mediated by anti-recombinant V antigen and
protein A-V antigen fusion peptide.
AU Motin V.L.; Nakajima R.; Smirnov G.B.; Brubaker R.R.
CS Department of Microbiology, Michigan State University,East Lansing, MI
48824, United States
SO Infection and Immunity, (1994) 62/10 (4192-4201).
ISSN: 0019-9567 CODEN: INFIBR
CY United States
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
037 Drug Literature Index
LA English
SL English

L14 ANSWER 105 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94105139 EMBASE
DN 1994105139
TI Mechanism of lymphocyte function-associated molecule 3-Ig fusion proteins
inhibition of T cell responses: Structure/function analysis in vitro and
in human CD2 transgenic mice.
AU Majeau G.R.; Meier W.; Jimmo B.; Kioussis D.; Hochman P.S.
CS Biogen, Inc., 14 Cambridge Center,Cambridge, MA 02142, United States
SO Journal of Immunology, (1994) 152/6 (2753-2767).
ISSN: 0022-1767 CODEN: JOIMA3
CY United States
DT Journal; Article
FS 026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
037 Drug Literature Index
LA English
SL English

L14 ANSWER 106 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94091699 EMBASE
DN 1994091699
TI Characterization of **domains** of herpes simplex virus type 1 glycoprotein E involved in Fc binding activity for **immunoglobulin G** aggregates.
AU Dubin G.; Basu S.; Mallory D.L.P.; Basu M.; Tal-Singer R.; Friedman H.M.

CS Infectious Diseases Division, 536 Johnson Pavilion, University of Pennsylvania,Philadelphia, PA 19104-6073, United States
SO Journal of Virology, (1994) 68/4 (2478-2486).
ISSN: 0022-538X CODEN: JOVIAM
CY United States
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
LA English
SL English

L14 ANSWER 107 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94362409 EMBASE
DN 1994362409
TI Recombinant thyrotropin receptor and the induction of autoimmune thyroid
disease in BALB/c mice: A new animal model.
AU Costagliola S.; Many M.C.; Stalmans-Falys M.; Tonacchera M.; Vassart G.;
Ludgate M.
CS IRIBHN, Universite Libre de Bruxelles, Campus Hopital Erasme, 808 route de
Lennik,B-1070 Brussel, Belgium
SO Endocrinology, (1994) 135/5 (2150-2159).
ISSN: 0013-7227 CODEN: ENDOAO
CY United States
DT Journal; Article
FS 003 Endocrinology
026 Immunology, Serology and Transplantation
037 Drug Literature Index
LA English
SL English

L14 ANSWER 108 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94273456 EMBASE
DN 1994273456
TI Expression of a fibrinolytically active human pro-urokinase fusion protein
in Escherichia coli.
AU Hua Z.; Jie L.; Zhu D.
CS Department of Biochemistry, Nanjing University,Nanjing 210008, China
SO Biochemistry and Molecular Biology International, (1994) 33/6 (1215-1220).
ISSN: 1039-9712 CODEN: BMBIES
CY Australia
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 109 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94160331 EMBASE
DN 1994160331
TI A single Fc binding **domain**-alkaline phosphatase gene fusion expresses a protein with both IgG binding ability and alkaline phosphatase
enzymatic activity.
AU Wang C.-L.; Huang M.; Wesson C.A.R.; Birdsell D.C.; Trumble W.R.

CS Dept of Bacteriology Biochemistry, University of Idaho,Moscow, ID 83844,
United States
SO Protein Engineering, (1994) 7/5 (715-722).
ISSN: 0269-2139 CODEN: PRENE
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 110 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94160330 EMBASE
DN 1994160330
TI Gene synthesis and functional expression of a protein exhibiting monodomain IgG Fc binding.
AU Trumble W.R.; Huang M.; West J.W.; Reasoner J.L.; Huang J.-L.; Wang C.-L.;
Douthart R.J.; Birdsell D.C.
CS Dept Bacteriology and Biochemistry, University of Idaho,Moscow, ID 83844,
United States
SO Protein Engineering, (1994) 7/5 (705-713).
ISSN: 0269-2139 CODEN: PRENE
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 111 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94122545 EMBASE
DN 1994122545
TI Frequent and early HIV-1(MN) neutralizing capacity in sera from Dutch HIV-
1 seroconverters is related to antibody reactivity to peptides from the
gp120 V3 **domain**.
AU Zwart G.; Back N.K.T.; Ramautarsing C.; Valk M.; Van der Hoek L.; Goudsmit
J.
CS Department of Virology, Academic Medical Center, Meibergdreef 15,1105 AZ
Amsterdam, Netherlands
SO AIDS Research and Human Retroviruses, (1994) 10/3 (245-251).
ISSN: 0889-2229 CODEN: ARHRE7
CY United States
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
LA English
SL English

L14 ANSWER 112 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 95021986 EMBASE
DN 1995021986
TI Construction and characterization of M13 bacteriophages displaying

functional IgG-binding **domains** of Staphylococcal protein A.
AU Kushwaha A.; Chowdhury P.S.; Arora K.; Abrol S.; Chaudhary V.K.
CS Department of Biochemistry, University of Delhi South Campus, Benito
Juarez Road,New Delhi 110021, India
SO Gene, (1994) 151/1-2 (45-51).
ISSN: 0378-1119 CODEN: GENED6
CY Netherlands
DT Journal; Article
FS 004 Microbiology
LA English
SL English

L14 ANSWER 113 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 5
AN 95051539 EMBASE
DN 1995051539
TI Construction of a bifunctional protein with IgG- and cellulose-binding
activities.
AU Kyaw C.M.; Araujo R.C.; De Valencia F.F.; Felipe M.S.S.; Astolfi-Filho S.
CS Departamento de Biologia Celular, Universidade de Brasilia,Brasilia-DF,
Brazil
SO Bioresource Technology, (1994) 50/1 (31-35).
ISSN: 0960-8524 CODEN: BIRTEB
CY United Kingdom
DT Journal; Conference Article
FS 004 Microbiology
029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 114 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 93207289 EMBASE
DN 1993207289
TI A soluble divalent class I major histocompatibility complex molecule
inhibits alloreactive T cells at nanomolar concentrations.
AU Porto J.D.; Johansen T.E.; Catipovic B.; Parfiit D.J.; Tuveson D.; Gether
U.; Kozlowski S.; Fearon D.T.; Schneck J.P.
CS Division of Clinical Immunology, Department of Medicine, Johns Hopkins
Univ. Sch. of Medicine,Baltimore, MD 21224, United States
SO Proceedings of the National Academy of Sciences of the United States of
America, (1993) 90/14 (6671-6675).
ISSN: 0027-8424 CODEN: PNASA6
CY United States
DT Journal; Article
FS 026 Immunology, Serology and Transplantation
LA English
SL English

L14 ANSWER 115 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 93129649 EMBASE
DN 1993129649

TI Molecular mechanisms underlying lymphocyte recirculation: III. Characterization of the LECAM-1 (L-selectin)-dependent adhesion pathway in rats.
AU Tamatani T.; Kuida K.; Watanabe T.; Koike S.; Miyasaka M.
CS Department of Immunology, Tokyo Metropolitan Inst. of Med. Sci, 3-18-22, Hon-Komagome,Bunkyo-ku, Tokyo 113, Japan
SO Journal of Immunology, (1993) 150/5 (1735-1745). ISSN: 0022-1767 CODEN: JOIMA3
CY United States
DT Journal; Article
FS 026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 116 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94039286 EMBASE
DN 1994039286
TI Characterization of a fusion protein composed of the extracellular **domain** of c-kit and the Fc region of human IgG expressed in a baculovirus system.
AU Liu Y.-C.; Kawagishi M.; Kameda R.; Ohashi H.
CS La Jolla Allergy/Immunology Inst., 11149 N. Torrey Pines Road,San Diego, CA 92037, United States
SO Biochemical and Biophysical Research Communications, (1993) 197/3 (1094-1102). ISSN: 0006-291X CODEN: BBRCA
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 117 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 93348913 EMBASE
DN 1993348913
TI Purification of fusion proteins using affinity microspheres in aqueous two-phase systems.
AU Kondo A.; Kaneko T.; Higashitani K.
CS Applied Chemistry Department, Kyushu Institute of Technology, Sensuicho,Tobata 804, Japan
SO Applied Microbiology and Biotechnology, (1993) 40/2-3 (365-369). ISSN: 0175-7598 CODEN: AMBIDG
CY Germany
DT Journal; Article
FS 004 Microbiology
LA English
SL English

L14 ANSWER 118 OF 130 USPATFULL
AN 92:86879 USPATFULL
TI Immunoassays for antibody to human immunodeficiency virus using recombinant antigens
IN Luciw, Paul A., Davis, CA, United States

Dina, Dino, San Francisco, CA, United States
PA Chiron Corporation, Emeryville, CA, United States (U.S. corporation)
PI US 5156949 19921020
AI US 1987-138894 19871224 (7)
RLI Continuation-in-part of Ser. No. US 1985-773447, filed on 6 Sep 1985,
now abandoned which is a continuation-in-part of Ser. No. US 1985-696534, filed on 30 Jan 1985, now abandoned which is a continuation-in-part of Ser. No. US 1984-667501, filed on 31 Oct 1984,
now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Nucker, Christine M.; Assistant Examiner: Woodward, M.
P.
LREP Blackburn, Robert P., McClung, Barbara G., Shetka, Debra A.
CLMN Number of Claims: 22
ECL Exemplary Claim: 1
DRWN 61 Drawing Figure(s); 59 Drawing Page(s)
LN.CNT 4178
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L14 ANSWER 119 OF 130 USPATFULL
AN 92:72398 USPATFULL
TI Construction of an IgG binding protein to facilitate downstream processing using protein engineering
IN Abrahmsen, Lars, Stockholm, Sweden
Moks, Tomas, Taby, Sweden
Nilsson, Bjorn, Sollentuna, Sweden
Uhlen, Mathias, Upsala, Sweden
PA KabiGen AB, Stockholm, Sweden (non-U.S. corporation)
PI US 5143844 19920901
AI US 1990-594564 19901009 (7)
PRAI SE 1985-5922 19851213
DT Utility
FS Granted
EXNAM Primary Examiner: Lacey, David L.; Assistant Examiner: Ulm, John D.
LREP Burns, Doane, Swecker, & Mathis
CLMN Number of Claims: 30
ECL Exemplary Claim: 1
DRWN 9 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 616
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L14 ANSWER 120 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 93014031 EMBASE
DN 1993014031
TI Expression and characterization of hepatocyte growth factor receptor-IgG
fusion proteins. Effects of mutations in the potential proteolytic
cleavage site on processing and ligand binding.
AU Mark M.R.; Lokker N.A.; Zioncheck T.F.; Luis E.A.; Godowski P.J.
CS Dept. of Molecular Biology, Genentech, Inc., 460 Point San Bruno Blvd.,South San Francisco, CA 94080, United States
SO Journal of Biological Chemistry, (1992) 267/36 (26166-26171).

ISSN: 0021-9258 CODEN: JBCHA3
CY United States
DT Journal; Article
FS 022 Human Genetics
026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 121 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 92364670 EMBASE
DN 1992364670
TI Identification of a pathogenic epitope involved in initiation of Heymann
nephritis.
AU Kerjaschki D.; Ullrich R.; Diem K.; Pietromonaco S.; Orlando R.A.;
Farquhar M.G.
CS Cancer Center, University of New Mexico,Albuquerque, NM 87131, United
States
SO Proceedings of the National Academy of Sciences of the United States of
America, (1992) 89/23 (11179-11183).
ISSN: 0027-8424 CODEN: PNASA6
CY United States
DT Journal; Article
FS 026 Immunology, Serology and Transplantation
028 Urology and Nephrology
LA English
SL English

L14 ANSWER 122 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 92223757 EMBASE
DN 1992223757
TI GMP-140 (P-selectin/CD62) binds to chronically stimulated but not resting
CD4+ T lymphocytes and regulates their production of proinflammatory
cytokines.
AU Damle N.K.; Klussman K.; Dietsch M.T.; Mohagheghpour N.; Aruffo A.
CS Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First
Avenue,Seattle, WA 98121, United States
SO European Journal of Immunology, (1992) 22/7 (1789-1793).
ISSN: 0014-2980 CODEN: EJIMAF
CY Germany
DT Journal; Article
FS 005 General Pathology and Pathological Anatomy
026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
037 Drug Literature Index
LA English
SL English

L14 ANSWER 123 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 92201702 EMBASE
DN 1992201702

TI Use of enzyme-linked immunosorbent assays with chimeric fusion proteins to
titrate antibodies against Epstein-Barr virus nuclear antigen 1.
AU Inoue N.; Kuranari J.; Harada S.; Nakajima H.; Ohbayashi M.; Nakamura Y.;
Miyasaka N.; Ezawa K.; Ban F.; Yanagi K.
CS Dept. of Virology and Rickettsiology, National Institute of Health,Tokyo,
Japan
SO Journal of Clinical Microbiology, (1992) 30/6 (1442-1448).
ISSN: 0095-1137 CODEN: JCMIDW
CY United States
DT Journal; Article
FS 004 Microbiology
029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 124 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 92286878 EMBASE
DN 1992286878
TI Autoantibodies against the amino-terminal cadherin-like binding
domain of pemphigus vulgaris antigen are pathogenic.
AU Amagai M.; Karpati S.; Prussick R.; Klaus-Kovtun V.; Stanley J.R.
CS Dermatology Branch, National Cancer Institute, National Institutes of
Health,Bethesda, MD 20892, United States
SO Journal of Clinical Investigation, (1992) 90/3 (919-926).
ISSN: 0021-9738 CODEN: JCINAO
CY United States
DT Journal; Article
FS 005 General Pathology and Pathological Anatomy
013 Dermatology and Venereology
026 Immunology, Serology and Transplantation
LA English
SL English

L14 ANSWER 125 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 92242988 EMBASE
DN 1992242988
TI A method for the evaluation of the efficiency of signal sequences for
secretion and correct N-terminal processing of human parathyroid hormone
produced in Escherichia coli.
AU Kareem B.N.; Rokkones E.; Hogset A.; Holmgren E.; Gautvik K.M.
CS Institute of Medical Biochemistry, University of Oslo,Oslo, Norway
SO Analytical Biochemistry, (1992) 204/1 (26-33).
ISSN: 0003-2697 CODEN: ANBCA2
CY United States
DT Journal; Article
FS 003 Endocrinology
004 Microbiology
029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 126 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.

AN 92040344 EMBASE
DN 1992040344
TI Extracellular **domain**-IgG fusion proteins for three human natriuretic peptide receptors: Hormone pharmacology and application to solid phase screening of synthetic peptide antisera.
AU Bennett B.D.; Bennett G.L.; Vitangcol R.V.; Jewett J.R.S.; Burnier J.; Henzel W.; Lowe D.G.
CS Dept. of Molecular Biology, Genentech, Inc., 460 Point San Bruno Blvd.,San Francisco, CA 94080, United States
SO Journal of Biological Chemistry, (1991) 266/34 (23060-23067). ISSN: 0021-9258 CODEN: JBCHA3
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 127 OF 130 BIOSIS COPYRIGHT 2002 BIOSIS
AN 1991:342266 BIOSIS
DN BA92:41641
TI EFFICIENT EXPRESSION OF A TRYPANOSOMA-CRUZI ANTIGEN IN ESCHERICHIA-COLI AND STAPHYLOCOCCUS-AUREUS AND ITS RAPID PURIFICATION.
AU MORENO J I; SEIGELCHIFER M; ZORZOPULOS J
CS DEP. MOL. GENETICS, BIOSIDUS S.A., CONSTITUCION 4234, 1254 BUENOS AIRES, ARGENTINA.
SO WORLD J MICROBIOL BIOTECHNOL, (1991) 7 (3), 316-323. CODEN: WJMBEY. ISSN: 0959-3993.
FS BA; OLD
LA English

L14 ANSWER 128 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 6
AN 91289404 EMBASE
DN 1991289404
TI Protein A-streptokinase fusion protein for immunodetection of specific IgG antibodies.
AU Schmidt K.-H.; Klessen C.; Kohler W.; Malke H.
CS Inst. Mikrobiologie/Exp. Ther., Beutenbergstr. 11,D-6900 Jena, Germany
SO Journal of Immunological Methods, (1991) 143/1 (111-117). ISSN: 0022-1759 CODEN: JIMMBG
CY Netherlands
DT Journal; Article
FS 026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
037 Drug Literature Index
LA English
SL English

L14 ANSWER 129 OF 130 BIOSIS COPYRIGHT 2002 BIOSIS
AN 1991:317905 BIOSIS
TI EXPRESSION IN ESCHERICHIA-COLI OF THE GENES CODING FOR REACTION CENTER

SUBUNITS FROM RHODOBACTER-SPHAEROIDES WILD-TYPE PROTEINS AND FUSION
PROTEINS CONTAINING ONE OR FOUR TRUNCATED **DOMAINS** FROM STAPHYLOCOCCUS-AUREUS PROTEIN A AT THE CARBOXY-TERMINUS.
AU SOEHLEMANN P; OECKL C; MICHEL H
CS LABORATORIUM MOLEKULARE BIOLOGIE, GENZENTRUM, AM KLOPFERSPITZ 18A, D-8033
MARTINSRIED, W. GER.
SO BIOCHIM BIOPHYS ACTA, (1991) 1089 (1), 103-112.
CODEN: BBACAQ. ISSN: 0006-3002.
FS BA; OLD
LA English

L14 ANSWER 130 OF 130 BIOSIS COPYRIGHT 2002 BIOSIS DUPLICATE 7
AN 1990:235460 BIOSIS
DN BA89:122413
TI AFFINITY IMMOBILIZATION OF A GENETICALLY ENGINEERED BIFUNCTIONAL **HYBRID PROTEIN**.
AU BANEYX F; SCHMIDT C; GEORGIOU G
CS DEP. CHEMICAL ENGINEERING, UNIV. TEXAS AT AUSTIN, AUSTIN, TEX. 78712.
SO ENZYME MICROB TECHNOL, (1990) 12 (5), 337-342.
CODEN: EMTED2. ISSN: 0141-0229.
FS BA; OLD
LA English

=> d bib 100-130

L14 ANSWER 100 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 95006043 EMBASE
DN 1995006043
TI Baculovirus-insect cell production of bioactive choriogonadotropin-
immunoglobulin G heavy-chain fusion proteins in sheep.
AU Johnson G.A.; Hansen T.R.; Austin K.J.; Van Kirk E.A.; Murdoch W.J.
CS Department of Animal Science, University of Wyoming,Laramie, WY 82071,
United States
SO Biology of Reproduction, (1995) 52/1 (68-73).
ISSN: 0006-3363 CODEN: BIREBV
CY United States
DT Journal; Article
FS 003 Endocrinology
026 Immunology, Serology and Transplantation
LA English
SL English

L14 ANSWER 101 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94366689 EMBASE
DN 1994366689
TI Regulation of p68 RNA helicase by calmodulin and protein kinase C.
AU Buelt M.K.; Glidden B.J.; Storm D.R.
CS Department of Pharmacology, University of Washington,Seattle, WA 98195,
United States

SO Journal of Biological Chemistry, (1994) 269/47 (29367-29370).
ISSN: 0021-9258 CODEN: JBCHA3
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
030 Pharmacology
037 Drug Literature Index
LA English
SL English

L14 ANSWER 102 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94306346 EMBASE
DN 1994306346
TI The disulfide linkages and glycosylation sites of the human natriuretic
peptide receptor-C homodimer.
AU Stults J.T.; O'Connell K.L.; Garcia C.; Wong S.; Engel A.M.; Garbers D.L.;
Lowe D.G.
CS Cardiovascular Research Department, Genentech, Inc.,South San Francisco,
CA 94080, United States
SO Biochemistry, (1994) 33/37 (11372-11381).
ISSN: 0006-2960 CODEN: BICHAW
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 103 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94186627 EMBASE
DN 1994186627
TI Expression and subcellular localization of poliovirus VPg-precursor
protein 3AB in eukaryotic cells: Evidence for glycosylation in vitro.
AU Datta U.; Dasgupta A.
CS Microbiology/Immunology Department, Jonsson Comprehensive Cancer Center,
University of California,Los Angeles, CA 90024-1747, United States
SO Journal of Virology, (1994) 68/7 (4468-4477).
ISSN: 0022-538X CODEN: JOVIAM
CY United States
DT Journal; Article
FS 004 Microbiology
LA English
SL English

L14 ANSWER 104 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94299231 EMBASE
DN 1994299231
TI Passive immunity to yersiniae mediated by anti-recombinant V antigen and
protein A-V antigen fusion peptide.
AU Motin V.L.; Nakajima R.; Smirnov G.B.; Brubaker R.R.
CS Department of Microbiology, Michigan State University,East Lansing, MI

48824, United States
SO Infection and Immunity, (1994) 62/10 (4192-4201).
ISSN: 0019-9567 CODEN: INFIBR
CY United States
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
037 Drug Literature Index
LA English
SL English

L14 ANSWER 105 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94105139 EMBASE
DN 1994105139
TI Mechanism of lymphocyte function-associated molecule 3-Ig fusion proteins
inhibition of T cell responses: Structure/function analysis in vitro and
in human CD2 transgenic mice.
AU Majeau G.R.; Meier W.; Jimmo B.; Kioussis D.; Hochman P.S.
CS Biogen, Inc., 14 Cambridge Center,Cambridge, MA 02142, United States
SO Journal of Immunology, (1994) 152/6 (2753-2767).
ISSN: 0022-1767 CODEN: JOIMA3
CY United States
DT Journal; Article
FS 026 Immunology, Serology and Transplantation
029 Clinical Biochemistry
037 Drug Literature Index
LA English
SL English

L14 ANSWER 106 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94091699 EMBASE
DN 1994091699
TI Characterization of **domains** of herpes simplex virus type 1 glycoprotein E involved in Fc binding activity for **immunoglobulin G** aggregates.
AU Dubin G.; Basu S.; Mallory D.L.P.; Basu M.; Tal-Singer R.; Friedman H.M.
CS Infectious Diseases Division, 536 Johnson Pavilion, University of Pennsylvania,Philadelphia, PA 19104-6073, United States
SO Journal of Virology, (1994) 68/4 (2478-2486).
ISSN: 0022-538X CODEN: JOVIAM
CY United States
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
LA English
SL English

L14 ANSWER 107 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94362409 EMBASE
DN 1994362409
TI Recombinant thyrotropin receptor and the induction of autoimmune thyroid
disease in BALB/c mice: A new animal model.
AU Costagliola S.; Many M.C.; Stalmans-Falys M.; Tonacchera M.; Vassart G.;

Ludgate M.
CS IRIBHN, Universite Libre de Bruxelles, Campus Hopital Erasme, 808 route de
Lennik,B-1070 Brussel, Belgium
SO Endocrinology, (1994) 135/5 (2150-2159).
ISSN: 0013-7227 CODEN: ENDOAO
CY United States
DT Journal; Article
FS 003 Endocrinology
026 Immunology, Serology and Transplantation
037 Drug Literature Index
LA English
SL English

L14 ANSWER 108 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94273456 EMBASE
DN 1994273456
TI Expression of a fibrinolytically active human pro-urokinase fusion protein
in Escherichia coli.
AU Hua Z.; Jie L.; Zhu D.
CS Department of Biochemistry, Nanjing University,Nanjing 210008, China
SO Biochemistry and Molecular Biology International, (1994) 33/6 (1215-1220).
ISSN: 1039-9712 CODEN: BMBIES
CY Australia
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 109 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94160331 EMBASE
DN 1994160331
TI A single Fc binding **domain**-alkaline phosphatase gene fusion expresses a protein with both IgG binding ability and alkaline phosphatase
enzymatic activity.
AU Wang C.-L.; Huang M.; Wesson C.A.R.; Birdsell D.C.; Trumble W.R.
CS Dept of Bacteriology Biochemistry, University of Idaho,Moscow, ID 83844,
United States
SO Protein Engineering, (1994) 7/5 (715-722).
ISSN: 0269-2139 CODEN: PRENE
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 110 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94160330 EMBASE
DN 1994160330
TI Gene synthesis and functional expression of a protein exhibiting monodomain IgG Fc binding.
AU Trumble W.R.; Huang M.; West J.W.; Reasoner J.L.; Huang J.-L.; Wang C.-L.;

Douthart R.J.; Birdsell D.C.
CS Dept Bacteriology and Biochemistry, University of Idaho,Moscow, ID 83844,
United States
SO Protein Engineering, (1994) 7/5 (705-713).
ISSN: 0269-2139 CODEN: PRENE
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 111 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 94122545 EMBASE
DN 1994122545
TI Frequent and early HIV-1(MN) neutralizing capacity in sera from Dutch HIV-
1 seroconverters is related to antibody reactivity to peptides from the
gp120 V3 **domain**.
AU Zwart G.; Back N.K.T.; Ramautarsing C.; Valk M.; Van der Hoek L.; Goudsmit
J.
CS Department of Virology, Academic Medical Center, Meibergdreef 15,1105 AZ
Amsterdam, Netherlands
SO AIDS Research and Human Retroviruses, (1994) 10/3 (245-251).
ISSN: 0889-2229 CODEN: ARHRE7
CY United States
DT Journal; Article
FS 004 Microbiology
026 Immunology, Serology and Transplantation
LA English
SL English

L14 ANSWER 112 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 95021986 EMBASE
DN 1995021986
TI Construction and characterization of M13 bacteriophages displaying
functional IgG-binding **domains** of Staphylococcal protein A.
AU Kushwaha A.; Chowdhury P.S.; Arora K.; Abrol S.; Chaudhary V.K.
CS Department of Biochemistry, University of Delhi South Campus, Benito
Juarez Road,New Delhi 110021, India
SO Gene, (1994) 151/1-2 (45-51).
ISSN: 0378-1119 CODEN: GENED6
CY Netherlands
DT Journal; Article
FS 004 Microbiology
LA English
SL English

L14 ANSWER 113 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 5
AN 95051539 EMBASE
DN 1995051539
TI Construction of a bifunctional protein with IgG- and cellulose-binding

activities.
AU Kyaw C.M.; Araujo R.C.; De Valencia F.F.; Felipe M.S.S.; Astolfi-Filho S.
CS Departamento de Biologia Celular, Universidade de Brasilia,Brasilia-DF,
Brazil
SO Bioresource Technology, (1994) 50/1 (31-35).
ISSN: 0960-8524 CODEN: BIRTEB
CY United Kingdom
DT Journal; Conference Article
FS 004 Microbiology
029 Clinical Biochemistry
LA English
SL English

L14 ANSWER 114 OF 130 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
AN 93207289 EMBASE
DN 1993207289
TI A soluble divalent class I major histocompatibility complex molecule
inhibits alloreactive T cells at nanomolar concentrations.
AU Porto J.D.; Johansen T.E.; Catipovic B.; Parfiit D.J.; Tuveson D.; Gether
U.; Kozlowski S.; Fearon D.T.; Schneck J.P.
CS Division of Clinical Immunology, Department of Medicine, Johns Hopkins
Univ. Sch. of Medicine,Baltimore, MD 21224, United States
SO Proceedings of the National Academy of Sciences of the United States of
America, (1993) 90/14 (6671-6675).
ISSN: 0027-8424 CODEN: PNASA6
CY United States
DT Journal; Article
<------User Break------>

FS 026 Immunology, Serology and Transplantationu
TI Molecular mechanisms underlying lymphocyte recirculation: III.
Characterization of the LECAM-1 (L-selectin)-dependent adhesion pathway in
rats.
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=> d his

(FILE 'HOME' ENTERED AT 15:58:56 ON 18 JAN 2002)

FILE 'EMBASE, MEDLINE, BIOSIS, USPATFULL, JAPIO, WPIDS, CAPLUS, AGRICOLA,
LIFESCI, BIOTECHDS, JICST-EPLUS' ENTERED AT 15:59:04 ON 18 JAN 2002
E BJORCK LARS/AU
L1 532 S E1-E4
E SJOBRING ULF/AU
L2 151 S E2-E3
L3 614 S L1-L2
L4 233 S L3 AND IMMUNOGLOBULIN?
L5 102 S L4 AND (PROTEIN L OR LIGHT CHAIN OR HYBRID)
L6 62 S L5 AND DOMAIN?
L7 24 DUP REM L6 (38 DUPLICATES REMOVED)

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L8        39787 S IMMUNOGLOBULIN? AND (PROTEIN L OR LIGHT CHAIN OR
HYBRID)
L9         9085 S L8 AND DOMAIN?
L10         850 S L9 AND IMMUNOGLOBULIN G
L11          42 S L10 AND PROTEIN L
L12          31 DUP REM L11 (11 DUPLICATES REMOVED)
L13         143 S L10 AND HYBRID PROTEIN
L14         130 DUP REM L13 (13 DUPLICATES REMOVED)

=> s l14 and domain?

L15         130 L14 AND DOMAIN?
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